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From: Saidha, Tekchand  
 Sent: Tuesday, March 04, 2003 4:00 PM  
 To: STIC-Biotech/ChemLib  
 Subject: 10/017145 - sequence search request

**10/017145 - sequence search request**

Please search the data bases and Interference files for :

SEQ ID NO : 1

Thank you,

*Tekchand Saidha  
 Primary Examiner  
 Art Unit 1652, CMM, Room No. 10D05  
 Mail Box 10D01  
 (703) 305-6595*

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MAR - 4 2003

STIC-BIOTECH/CH/SLIB  
 (STIC)

Point of Contact  
 P. Sheppard

Telephone number: (703) 308-4499

Searcher: \_\_\_\_\_  
 Phone: \_\_\_\_\_  
 Location: \_\_\_\_\_  
 Date Picked Up: \_\_\_\_\_  
 Date Completed: 3/7/03  
 Searcher Prep/Review: \_\_\_\_\_  
 Clerical: \_\_\_\_\_  
 Online time: \_\_\_\_\_

TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
 AA Sequences: \_\_\_\_\_  
 Structures: \_\_\_\_\_  
 Bibliographic: \_\_\_\_\_  
 Litigation: \_\_\_\_\_  
 Full text: \_\_\_\_\_  
 Patent Family: \_\_\_\_\_  
 Other: \_\_\_\_\_

VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
 DIALOG: \_\_\_\_\_  
 Questel/Orbit: \_\_\_\_\_  
 DRLink: \_\_\_\_\_  
 Lexis/Nexis: \_\_\_\_\_  
 Sequence Sys.: \_\_\_\_\_  
 WWW/Internet: \_\_\_\_\_  
 Other (specify): \_\_\_\_\_

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Result No.	Score	Query Match	Length	DB	ID	Description
1	1771	92.4	396	10	Q43140	043140 sesamum ind
2	1757	91.7	396	10	Q43141	043141 sesamum ind
3	1746	91.1	396	10	Q93X20	093X20 sesamum ind
4	1733	90.4	401	10	Q22832	022832 arabidopsis
5	1729	90.2	401	10	Q94A99	094A99 arabidopsis
6	1727	90.1	396	10	Q24497	024497 helianthus
7	1701	88.8	396	10	Q43140	024498 helianthus
8	1698	88.6	396	10	Q9SEK6	09SEK6 persica amer
9	1698	88.6	401	10	Q39355	093X55 brassica napus
10	1676.5	88.5	409	10	Q9SW87	09SW87 arachis hyp
11	1695	88.5	401	8	Q9XQR7	09XQR7 brassica juncea
12	1688	88.1	396	10	Q65040	065040 mactafadiyana
13	1673	87.3	396	10	Q8VXJ7	08VXJ7 helianthus
14	1670	87.2	396	10	Q8VXJ8	08VXJ8 helianthus
15	1660.5	86.7	407	10	Q42591	042591 arabidopsis
16	1653.5	86.3	396	10	Q8S059	08S059 oryza sativ

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Scoring table: BIOSUM62	Gapext 10.0	Gapext 0.5	RESULT 1	PRELIMINARY;	PRT;	396 AA.
Searches: 671580 seqs, 206047115 residues			Q43140	ID Q43140;		
Total number of hits satisfying chosen parameters: 671580			AC	AC		
Minimum DB seq length: 0			DT 01-NOV-1996 (TREMBLref. 01, Created)	DT 01-NOV-1996 (TREMBLref. 01, Last sequence update)		
Maximum DB seq length: 2000000000			33 1219.5	63.6	401	10 Q9LF05
Post-processing: Minimum Match 0%			34 1218	63.6	10	Q9MB79
Maximum Match 100%			35 1009.5	52.7	222	10 Q9MB80
Listing first 45 summaries			36 771	40.2	167	10 Q9xFL1
Database : SPTREMBL 21;*			37 745	38.9	161	10 Q9XF81
1: sp_archaea;*			38 307	16.0	328	16 Q9XAL3
2: sp_bacteria;*			39 272	14.2	338	16 Q9VKD4
3: sp_fungi;*			40 272	14.2	338	16 Q50824
4: sp_human;*			41 267	13.9	338	16 Q50050
5: sp_invertebrate;*			42 158	8.2	275	16 Q9x793
6: sp_mammal;*			43 142	7.4	170	2 Q98539
7: sp_mhc;*			44 138	7.2	275	16 Q53442
8: sp_organelle;*			45 126.5	6.6	1349	5 Q9VPR5
9: sp_phage;*						
10: sp_plant;*						
11: sp_rabbit;*						
12: sp_virus;*						
13: sp_vertebrate;*						
14: sp_unclassified;*						
15: sp_rvirus;*						
16: sp_bacteriopl;						
17: sp_archeap;*						

Scoring table: BIOSUM62	Gapext 10.0	Gapext 0.5	RESULT 1	PRELIMINARY;	PRT;	396 AA.
Searches: 671580 seqs, 206047115 residues			Q43140	ID Q43140;		
Total number of hits satisfying chosen parameters: 671580			AC	AC		
Minimum DB seq length: 0			DT 01-NOV-1996 (TREMBLref. 01, Created)	DT 01-NOV-1996 (TREMBLref. 01, Last sequence update)		
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Searches: 671580 seqs, 206047115 residues			Q43140	ID Q43140;		
Total number of hits satisfying chosen parameters: 671580			AC	AC		
Minimum DB seq length: 0			DT 01-NOV-1996 (TREMBLref. 01, Created)	DT 01-NOV-1996 (TREMBLref. 01, Last sequence update)		
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Searches: 671580 seqs, 206047115 residues			Q43140	ID Q43140;		
Total number of hits satisfying chosen parameters: 671580			AC	AC		
Minimum DB seq length: 0			DT 01-NOV-1996 (TREMBLref. 01, Created)	DT 01-NOV-1996 (TREMBLref. 01, Last sequence update)		
Maximum DB seq length: 2000000000			33 1219.5	63.6	401	10 Q9LF05
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Scoring table: BIOSUM62	Gapext 10.0	Gapext 0.5	RESULT 1	PRELIMINARY;	PRT;	396 AA.
Searches: 671580 seqs, 206047115 residues			Q43140	ID Q43140;		
Total number of hits satisfying chosen parameters: 671580			AC	AC		
Minimum DB seq length: 0			DT 01-NOV-1996 (TREMBLref. 01, Created)	DT 01-NOV-1996 (TREMBLref. 01, Last sequence update)		
Maximum DB seq length: 2000000000			33 1219.5	63.6	401	10 Q9LF05
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6: sp_mammal;*			43 142	7.4	170	2 Q98539
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9: sp_phage;*						
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15: sp_rvirus;*						
16: sp_bacteriopl;						
17: sp_archeap;*						

Scoring table: BIOSUM62	Gapext 10.0	Gapext 0.5	RESULT 1	PRELIMINARY;	PRT;	396 AA.
Searches: 671580 seqs, 206047115 residues			Q43140	ID Q43140;		
Total number of hits satisfying chosen parameters: 671580			AC	AC		
Minimum DB seq length: 0			DT 01-NOV-1996 (TREMBLref. 01, Created)	DT 01-NOV-1996 (TREMBLref. 01, Last sequence update)		
Maximum DB seq length: 2000000000			33 1219.5	63.6	401	10 Q9LF05
Post-processing: Minimum Match 0%			34 1218	63.6	10	Q9MB79
Maximum Match 100%			35 1009.5	52.7	222	10 Q9MB80
Listing first 45 summaries			36 771			



RC	TISSUE-DEVELOPING SEED;	RN	[12]
RA	Chopra V.L.;	RP	SEQUENCE FROM N.A.
RT	"transgenic indian mustard high in oleate";	RC	STRAIN=CV. COLUMBIA;
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.	RA	Lin X.;
DR	EMBL: AJ31331; CAC4792-1; -.	RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR	InterPro: IPR005067; FA_desaturase.	RN	[13]
DR	InterPro: IPR001225; FA_desaturase_2; 1.	RP	SEQUENCE FROM N.A.
DR	PF03405; FA_desaturase_2; 1.	RA	Fachroo P. Shanklin J., Shah J., Whittle E.J., Klessig D.F.;
DR	PROSITE: PS00544; Fatty_acid_desaturase_2; 1.	RT	"FA fatty acid desaturase modulates the activation of defense signaling pathways in plants";
SQ	SEQUENCE: 450544 MW: 4945DFAC6687BB2 CRC64;	RL	Proc. Natl. Acad. Sci. U.S.A. 98: 9448-9453 (2001).
Query Match	91.1%; Score 1746; DB 10; Length 396;	CC	-1- FUNCTION: Converts Stearyl ACP to Oleoyl ACP by introduction of a cis double bond between carbons delta-9 and delta-10 of the acyl chain (by similarity).
Best Local Similarity	89.8%; Pred. No. 8.5e-135;	CC	-1- CATALYTIC ACTIVITY: Stearyl [acyl-carrier protein] + AH(2) + O(2) = Oleoyl-[acyl-carrier protein] + A + 2 H(2)o.
Matches	326; Conservative 21; Mismatches 16; Indels 0; Gaps 0;	CC	-1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).
Qy	1 ASTLRSGSKEVEENLKKPMPREVIQVTISMPKQIEKTSKLDWAEENLVLHKPKVEK 60	CC	-1- PATHWAY: Catalyzes the principal conversion of saturated fatty acids to unsaturated fatty acids in the synthesis of vegetable oils.
Db	34 ASTLRSGSKEVEETVKPKPENPREVQVTISMPKQIEKTSKLDWAEENLVLHKPKVEK 93	CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
Qy	61 CWQOPDPLPDAASGDEQRELRERAKEIPEDDYFVVLVGDMITEBALPPYQTMNLTG 120	CC	-1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
Db	94 CWQOPDPLPSSSDGDDQKELREAKEIPEDDYFVVLVGDMITEBALPPYQTMNLTG 153	CC	-1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
Qy	121 VRDETAGSPTSWAIWTRAAENRHDLLNKLYLGSRYDMRQEKTIOYLIGSGMDPR 180	CC	DR EMBL: AE395441; AAK85232; -.
Db	154 VRDETAGSPTSWAIWTRAAENRHDLLNKLYLGSRYDMRPNKGTFRLIGSGMDPR 213	DR	DR EMBL: AE395441; AAK85232; -.
Qy	181 TENSPPLYGFTTSQFRATFISHGNTPARQKEHGDIKLQAQCGTIAADERHETAYKIV 240	DR	DR EMBL: P22337; 1ARR.
Db	214 TENSPPLYGFTTSQFRATFISHGNTPARLAREHGDLKLQAQCGTIAADERHETAYKIV 273	DR	DR InterPro: IPR005067; FA_desat.
Qy	241 EKLFLIDPDTGYLFLADMMRKKISMPAHLYMDGRDNLFHDSAVAQRQLGYTTAKYADI 300	DR	DR InterPro: IPR001225; FA_desat.
Db	274 EKLFLIDPNTIVLFLADMMRKKISMPAHLYMDGRDNLFHDSAVAQRQLGYTTAKYADI 333	DR	DR Pfam: PF03405; FA_desat.
Qy	301 LEFLYGRWKVYDKLTLGLSAEGQKAQDYVCRFLPPIRRLEREAQGRAKEAPTMPSWLFDRQ 360	DR	DR PSSM: PS00574; Fatty_acid_desaturase_2; 1.
Db	334 LEHLVARWKVANLTGLSADGQKAQDYVCGLPPIRRLEREAQGRAKQAKP1PFSWVHDRE 393	DR	DR Chloroplast: Fatty acid biosynthesis; NADP; Oxidoreductase; KW transit peptide.
Qy	361 VKL 363	DR	DR Score 1733; DB 10; Length 401;
Db	394 VQL 396	DR	DR Best Local Similarity 89.4%; Pred. No. 1e-133; Mismatches 22; Indels 0; Gaps 0;
RESULT 4			
O22832	PRELIMINARY; PRT: 401 AA.	Qy	4 LKSGSKEVENLKKPMPREVIQVTISMPKQIEKTSKLDWAEENLVLHKPKVEKQWQ 63
AC	O22832; PRELIMINARY; PRT: 401 AA.	Db	42 LSSGPKEVSLKKPFTPREVQVQLHSMPPKQIEKSMENWAENLILHKDVERSWQ 101
DT	01-JAN-1998 (TREMBLrel. 05, Created)	Qy	64 PDDFLPDPASGDFDEVYRELREAKEIPEDDYFVVLVGDMITEALPPYQTMNLTGIVRD 123
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)	Db	102 PDDFLPDPASGDFDEVYRELREAKEIPEDDYFVVLVGDMITEALPPYQTMNLTGIVRD 161
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	Qy	124 ERGASPTSWAIWTRAAENRHDLLNKLYLGSRYDMRQEKTIOYLIGSGMDPTEN 183
DE	DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).	Db	162 ERGASPTSWAIWTRAAENRHDLLNKLYLGSRYDMRQEKTIOYLIGSGMDPTEN 221
GN	GN 24310 or S12.	Qy	184 SPYLGFIYTSQFRATFISHGNTPARQKEHGDIKLQAQCGTIAADERHETAYKIVEKL 243
OS	Arabidopsis thaliana (Mouse-ear cress).	Db	222 NPYLGFIYTSQFRATFISHGNTPARQKEHGDIKLQAQCGTIAADERHETAYKIVEKL 281
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosidae II; Brassicales; Brassicaceae; Arabidopsis.	Qy	244 FEIDPDTGYLFLADMMRKKISMPAHLYMDGRDNLFHDSAVAQRQLGYTTAKYADILEF 303
OC	NCBI_TAXID=3702;	Db	282 FEIDPDTGYLFLADMMRKKISMPAHLYMDGRDNLFHDSAVAQRQLGYTTAKYADILEF 341
RN	[1]	Qy	304 LVGRWKVYDKLTLGLSAEGQKAQDYVCRFLPPIRRLEREAQGRAKEAPTMPSWLFDRQVYL 363
RP	SEQUENCE FROM N.A.	Db	342 LVGRWKVYDKLTLGLSAEGQKAQDYVCRFLPPIRRLEREAQGRAKEAPTMPSWLFDRQVYL 401
RC	STRAIN=CV. COLUMBIA;	RESULT 5	RESULTS 5
RX	MBIDLINE=20083487; PubMed=10617197;	Q94AE9	Q94AE9; PRELIMINARY;
RA	RA 1. Kaul S., Rounse S.D., Shea T.P., Benito M.-I., Town C.D.,	AC	AC Q94AE9; PRELIMINARY;
RA	RA Fuji C.Y., Mason T.M., Bowman C.S., Barnstead M.E., Feldblum T.V.,	DT	DT 01-DEC-2001 (TREMBLrel. 19, Created)
RA	RA Bueli C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,	DT	DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
RA	RA Cronin L.A., Shen M., Vanam S.E., Umavam L., Tallon L.J., Gill J.E.,	DT	DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
RA	RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,	DE	DE AT2943710/F18019.18.
RA	RA Copenhafer G.P., Preuss D., Nieman W.C., White O., Eisen J.A.,		
RA	RA Salzberg S.L., Fraser C.M., Venter J.C.;		
RT	RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";		
RT	RT Nature 402:761-768 (1999).		

OS Arabidopsis thaliana (Mouse-ear cress); Embryophyta; Tracheophyta; Embryophyta; Streptophyta; Embryophyta; Tracheophyta; Embryophyta; core eudicots; Rosidae; Eukaryota; Viridiplantae; eu dicotyledons; core eudicots; OC spermatophyta; Magnoliophyta; eu dicotyledons; Brassicaceae; Arabidopsis; NCBI\_TaxID=3702;

RN [1]

SEQUENCE FROM N.A.

RA Koesema E., Chen H., Cheuk R., Kim C.J., Meyers M.C., Shinn P., Banh J., Bowser L., Carninci P., Dale J.M., Gibson H.A., Jones T., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Neumann M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Narusawa M., Onodera C.S., Palm C.J., Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K., RA "Arabidopsis cDNA clones.";

RT "Theologis A.," Ecker J.R., Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

[2]

RP SEQUENCE FROM N.A.

RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J., Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Narusawa M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R., "Arabidopsis ORF clones.";

RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY048233; AAB82496; 1; -.

DR EMBL; AY04014; AAM16170; 1; -.

DR InterPro; IPR005067; FA\_desaturase.

DR InterPro; IPR001225; FA\_desaturase.

DR PFam; PF03405; FA\_desaturase\_2; 1.

DR PROSITE; PS00574; FA\_ACID\_DESATURASE.

DR SEQUENCE; 401 AA; 45692 MW; O1F09DD370F4E1D1 CRC64;

Query Match 90.2%; Score 1729; DB 10; Length 401; Best Local Similarity 89.2%; Pred. No. 2.e-133; Matches 321; Conservative 23; Mismatches 16; Indels 0; Gaps 0;

QY 4 LKSGSKREVNLLKKPMPREHVQVTHSMPPQKIEFKSLDWAENBILVHLKPVEKWCQ 63

DB 42 LSSGPKEVSKLKKPMPREHVQVLSHSMPPQKIEFKSMENVAEENLILHLKDVKESWQ 101

QY 64 EQDFLDPSAGFDECYRETRERKEIIPDDYFVVLGDMTEALPTQMLNLTDGYRD 123

DB 102 EQDFLDPSAGFDECYRETRERKEIIPDDYFVVLGDMTEALPTQMLNLTDGYRD 161

QY 124 ETGASPTSWA1WTRAWTAEEENRIGDILNKLYLSSGRVDMRQIEKTIQYLGSQMDPRTEN 183

DB 162 ETGASPTSWA1WTRAWTAEEENRIGDILNKLYLSSGRVDMRQIEKTIQYLGSQMDPRTEN 221

QY 184 SPYLGFTYTSQERATFISHGNTARQAKENGDIKLAQICGTADEKRHETAYTKIVEKL 243

DB 222 NPYLGFTYTSQERATFISHGNTARQAKENGDIKLAQICGTADEKRHETAYTKIVEKL 281

QY 244 FFLIDPDGTVLAFADMRRKTSMPAHYMDGRDNLDHSAVAQRLGVHTAKDYLDEF 303

DB 282 FFLIDPDGTVMFADMRRKTSMPAHYMDGRDNLDNFNSSAVAQRLGVHTAKDYLDEF 341

QY 304 LVGRWKVDKLGLSAEGQKAOQDYVCRLLPPIRRLERQAQRAKEAPTMPFWSIFDQYKL 363

DB 342 LVGRWKVQDLDLGLSGBSNKACDYLGLAPR1KRLDEAQRAKGPKIPFSWHDREVQ 401

Query Match 90.1%; Score 1727; DB 10; Length 396; Best Local Similarity 88.7%; Pred. No. 3.e-133; Matches 322; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

QY 1 ASTLKGSGSKREVNLLKKPMPREHVQVTHSMPPQKIEFKSLDWAENBILVHLKPVEK 60

DB 34 ASTLKGSSPKVESTKPKTPPREGHQLQVTHSMPPQKIEFKSFGWAEDNLVHLKPVEK 93

Query Match 90.1%; Score 1727; DB 10; Length 396; Best Local Similarity 88.7%; Pred. No. 3.e-133; Matches 322; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

QY 1 ASTLKGSGSKREVNLLKKPMPREHVQVTHSMPPQKIEFKSLDWAENBILVHLKPVEK 60

DB 94 CWOQDFPPEPASGFECKYKLRABEIPDYEYVVLGDMTEAALPTQMLNLTDGY 153

QY 121 VRDETGASPTSWA1WTRAWTAEEENRIGDILNKLYLSSGRVDMRQIEKTIQYLGSQMDPRTEN 180

DB 154 VRDETGASPTPWAWTRAWTAEEENRIGDILNKLYLSSGRVDMRQIEKTIQYLGSQMDPRTEN 213

QY 181 TENSPLYGFYTSQERATFISHGNTARQAKENGDIKLAQICGTADEKRHETAYTKIV 240

DB 214 TENSPLYGFYTSQERATFISHGNTARQAKENGDIKLAQICGTADEKRHETAYTKIV 273

QY 241 EKLFIDPDGTVLAFADMRRKTSMPAHYMDGRDNLDHSAVAQRLGVHTAKDYLDEF 300

DB 274 EKLFIDPDGTVLAFADMRRKTSMPAHYMDGRDNLDHSAVAQRLGVHTAKDYLDEF 333

QY 301 LEFLVGRWKVQDLDLGLSGBSNKACDYLGLAPR1KRLDEAQRAKGPKIPFSWHDREVQ 360

DB 334 LEFLVGRWKVQDLDLGLSGBSNKACDYLGLAPR1KRLDEAQRAKGPKIPFSWHDREVQ 393

QY 361 VKL 363

DB 394 VKL 396

RESULT 6  
O24497  
ID O24497  
AC 024497;  
DT 01-JAN-1998 (TRIMBLrel. 05, Created 01-JAN-1998 (TRIMBLrel. 05, Last sequence update 01-JUN-2002 (TRIMBLrel. 21, Last annotation update)

RESULT 7  
O24498  
ID O24498

AC	024498;	RESULT: 8
DT	01-JAN-1998 (TREMBLref. 05, Created)	09SEK6
DT	01-JAN-1998 (TREMBLref. 05, Last sequence update)	PRELIMINARY;
DT	01-JUN-2002 (TREMBLref. 21, Last annotation update)	FRT;
DB	Acyl - acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).	09SEK6;
DE	Helianthus annuus (Common sunflower).	AC
OS	Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Asteroidae; Heliantheae; Helianthus.	DT 01-MAY-2000 (TREMBLref. 13, Created)
OC	Persea americana (Avocado).	DT 01-MAY-2000 (TREMBLref. 13, Last sequence update)
OC	Persea americana (Avocado).	DT 01-JUN-2002 (TREMBLref. 21, Last annotation update)
OX	NCBI_TaxID:4232;	DE Acyl - acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).
RN	[1]	DE
RP	SEQUENCE FROM N.A.	DE
RC	SEQUENCE FROM N.A.	DE
RA	Hongrakul V., Slabough M.B., Knapp S.J.;	RP=SEQUENCE FROM N.A.
RT	Sunflower stearoyl-ACP desaturase;	STRAN=CV; FUELRE;
RL	Submitted (FEB-1997) to the ENBL/GenBank/DDJB databases.	RA
CC	-!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CTS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).	RA
CC	-!- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2) = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.	RT
CC	-!- COFACTOR: FERREDOXIN. FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).	RT
CC	-!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.	RT
CC	-!- SUBUNIT: HOMODIMER (BY SIMILARITY).	RT
CC	-!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).	RT
CC	-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.	RT
DR	EMBL: U91340; P22337; IAFR. HSSP: P22337; IAFR.	RT
DR	InterPro: IPR005067; FA_desat.	RT
DR	DR InterPro: IPR001225; FA_desat.	RT
DR	Pfam: PF03405; FA_desat.	RT
DR	PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.	RT
DR	Chloroplast; Fatty acid biosynthes; NADP; Oxidoreductase; KW	RT
DR	Chloroplast; Fatty acid biosynthes; NADP; Oxidoreductase; KW	RT
DR	Transit peptide.	RT
SQ	SEQUENCE 396 AA: 45112 MW; C9DB8CD04310BFAA CRC64;	RT
Query Match	88.48%; Score 1701; DB 10; Length 396;	RT
Best Local Similarity	88.48%; Pred. No. 4. 2e-131;	RT
Matches	321; Conservative 18; Mismatches 24; Indels 0; Gaps 0;	RT
Qy	1 ASTLKGSGKEVENLKKPMPREHYVOTHSMPPQKIEFKSLDNAAENILVHLKPVEK 60	Query Match 88.6%; Score 1698; DB 10; Length 396;
Db	34 ASTIGATTAKVESTRKPFPTPREHQVQLSMPPQKIEFKSLDNAAENILVHLKPVEK 93	Best Local Similarity 87.1%; Pred. No. 7. 3e-131; RT
Qy	61 CWQPQDFLPDASDGDFEQYRELREBKEIPDDYFVVLGDMITEALPYQTMLNTLG 120	RT
Db	94 CWAQDFLPDASDGDFEQYRELREBKEIPDDYFVVLGDMITEALPYQTMLNTLG 153	RT
Qy	121 VRDETGASPTSWAIWTRAWTAENRIGDLINKYLSGRDMQTEKTIOLIGSGMDPR 180	RT
Db	154 VRDETGASPTSWAIWTRAWTAENRIGDLINKYLSGRDMQTEKTIOLIGSGMDPR 213	RT
Qy	181 TENSPLGFYTSFQERATFISHGNTARQKEHGDYKLAQICGTAADEERHETAYTKIV 240	RT
Db	214 TENSPLGFYTSFQERATFISHGNTARHAKKEHGDYKLAQICGTAADEERHETAYTKIV 273	RT
Qy	241 EKLFEIDPDGTIVLAFADMRRKKISMPAHLYGDRDNLFENSAQRLGYTTADYADI 300	RT
Db	274 EKLFEIDPDGTIVLAFADMRRKKISMPAHLYGDRDNLFENSAQRLGYTTADYADI 333	RT
Qy	301 LEFLVGRWKVDKLGLSAEGQKAQDYCVRCLPRIRRLEREAQGRAKEAPTMPSWIFDQ 360	RT
Db	334 LEFLVGRWKVADLTLGSGERKAQDVCGLAQIRRLERNSARAKESVNVPFSWIFDQ 393	RT
Qy	361 VKL 363	RT
Db	394 VKL 396	RT
Qy	301 LEFLVGRWKVDKLGLSAEGQKAQDYCVRCLPRIRRLEREAQGRAKEAPTMPSWIFDQ 360	RT
Db	334 LEFLVGRWKVADLTLGSGERKAQDVCGLAQIRRLERNSARAKESVNVPFSWIFDQ 393	RT
Qy	1 ASTLKGSGKEVENLKKPMPREHYVOTHSMPPQKIEFKSLDNAAENILVHLKPVEK 60	Query Match 88.6%; Score 1698; DB 10; Length 396;
Db	34 ASTLRSSTKEDVNKKPFSPPREHVQVTHSMPPQKIEFKSLDNAAENILVHLKPVEK 93	Best Local Similarity 87.1%; Pred. No. 7. 3e-131; RT
Qy	61 CWQPQDFLPDASDGDFEQYRELREBKEIPDDYFVVLGDMITEALPYQTMLNTLG 120	RT
Db	94 CWAQDFLPDASDGDFEQYRELREBKEIPDDYFVVLGDMITEALPYQTMLNTLG 153	RT
Qy	121 VRDETGASPTSWAIWTRAWTAENRIGDLINKYLSGRDMQTEKTIOLIGSGMDPR 180	RT
Db	154 VRDETGASPTSWAIWTRAWTAENRIGDLINKYLSGRDMQTEKTIOLIGSGMDPR 213	RT
Qy	181 TENSPLGFYTSFQERATFISHGNTARQKEHGDYKLAQICGTAADEERHETAYTKIV 240	RT
Db	214 TENSPLGFYTSFQERATFISHGNTARHAKKEHGDYKLAQICGTAADEERHETAYTKIV 273	RT
Qy	241 EKLFEIDPDGTIVLAFADMRRKKISMPAHLYGDRDNLFENSAQRLGYTTADYADI 300	RT
Db	274 EKLFEIDPDGTIVLAFADMRRKKISMPAHLYGDRDNLFENSAQRLGYTTADYADI 333	RT
Qy	301 LEFLVGRWKVDKLGLSAEGQKAQDYCVRCLPRIRRLEREAQGRAKEAPTMPSWIFDQ 360	RT
Db	334 LEFLVGRWKVADLTLGSGERKAQDVCGLAQIRRLERNSARAKESVNVPFSWIFDQ 393	RT
Qy	361 VKL 363	RT
Db	394 VKL 396	RT

Qy	361	VKL	363	Db	282	LEIDPDGTVAFADEMRKKTSMPAHLMYGRDDKLFDNFSSVAQRLGVYTAKYADILEF
Db	394	VKL	396	Qy	304	LVGRWKVDKLTKLPSAEGQKAQDYVCLPPRTRRLERAGRAQRAKEAFTMPFWSIFRQVKL
RESULT 9				Db	342	LVGRWKVLSLSGCGNCNAQEYLCGLTPTRRLDRAQARAKKGPKIPFSWIDREVQL
Q39355	TD	Q39355	PRELIMINARY;	PRT;	401	AA.
AC	Q39355;			Q9SW87	PRELIMINARY;	PRT;
DT	01-NOV-1996	(TREMBLrel. 01, Created)		Q9SW87	409	AA.
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		AC	409	AA.
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		Q9SW87		
DE	Acyl-(lacy)-carrier protein	desaturase		ID	13;	Created)
DE	Acyl-(lacy)-carrier protein	desaturase		DT	13;	Created)
GN	BN4.			DT	13;	Created)
OS	Brassica napus (Rape).			DT	13;	Created)
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			DT	21;	Last sequence update
OC	Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta;			DT	21;	Last annotation update
OC	eurosid I; Brassicales; Brassicaceae; Brassica.			DE	21;	Last annotation update
OX	NCBI_TaxID=3708;			DE	21;	Last annotation update
RN	[1]			DE	21;	Last annotation update
RP	SEQUENCE FROM N.A.			DE	21;	Last annotation update
RC	RESTRAIN-CV: JET NEU;			DE	21;	Last annotation update
RX	MEDLINE=94:286739; PubMed=8016261;			DE	21;	Last annotation update
RA	Slocmbe S.P.; Piffanelli P., Fairbairn D., Bowra S., Hatzopoulos H.,			DE	21;	Last annotation update
RA	Tsiantis M., Murphy D.J.,			DE	21;	Last annotation update
RT	"Temporal and tissue specific regulation of a Brassica napus stearoyl- acyl carrier protein desaturase gene.";			DE	21;	Last annotation update
RT	Plant Physiol. 104:1167-1176 (1994).			DE	21;	Last annotation update
CC	-1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).			DE	21;	Last annotation update
CC	-1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2) -> OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.			DE	21;	Last annotation update
CC	-1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).			DE	21;	Last annotation update
CC	-1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.			DE	21;	Last annotation update
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).			DE	21;	Last annotation update
CC	-1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).			DE	21;	Last annotation update
CC	-1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.			DE	21;	Last annotation update
EMBL	X47822; CAA52786; 1.			DE	21;	Last annotation update
DR	HSSP; P22337; 1AFR.			DR	InterPro; IPR005037; FA_desat.	
DR	InterPro; IPR005067; FA_desat.			DR	InterPro; IPR001225; FA_desat.	
DR	PFam; PF03405; FA_desat.			DR	PFam; PF03405; FA_desat.	
DR	PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.			DR	PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.	
KW	Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;			KW	Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;	
KW	Transit peptide.			KW	Transit peptide.	
SEQUENCE	401 AA;	45482	MW;	1CCFB15626270401	CRC64;	;
SQ	88.6%; Score 1698; DB 10; Length 401;			SQ	409 AA;	46810 MW;
Query	Match	88.5%; Score 1696.5; DB 10; Length 409;		Query	1	ASTLKSGSKEVENLKKPFMPMPREHYVQTHSMPPQKIEFKSLDNWAENILVHLKPVEK 60
Best	Local	Similarity	86.7%; Pred. No. 7.5e-131;	Best	Local	Similarity
Matches	312;	Conservative	30; Mismatches 18;	Matches	319;	Conservative
0;	0;	0;	24;	Mismatches	20;	Indels
0;	0;	0;	3;	Gaps	1;	
4	LKGSGSKEVENLKKPFMPMPREHYVQTHSMPPQKIEFKSLDNWAENILVHLKPVEK 63			Db	44	ASTLKSGSKEVENLKKPFMPMPREHYVQTHSMPPQKIEFKSLDNWAENILVHLKPVEK 103
Db	42	LSSTSKKEVEKSLKKPFMPKKEVHQVLSHSMPPQKIEFKSLDNLTHLDEKSHQ	101	Qy	61	CWQPODFLPDPASDGFDEQYREKREKARKEIPDDYFVVLYGDMITEALALPYQTMLNTLG 120
Qy	64	PQDFLPDPASDGFDEQYREKREKARKEIPDDYFVVLYGDMITEALALPYQTMLNTLG 123		Qy	62	CWQPODFLPDPASDGFDEQYREKREKARKEIPDDYFVVLYGDMITEALALPYQTMLNTLG 163
Db	102	PQDFLPDPASDGFDEQYREKREKARKEIPDDYFVVLYGDMITEALALPYQTMLNTLG 161		Db	104	CWQPODFLPDPASDGFDEQYREKREKARKEIPDDYFVVLYGDMITEALALPYQTMLNTLG 163
Qy	124	ETGASPTSWATRANTAEERHRGDLINKLYLPSGRVDMRQIERTQYLIGSGMDPR	183	Qy	121	VRDETGAQSPSWATRANTAEERHRGDLINKLYLPSGRVDMRQIERTQYLIGSGMDPR
Db	162	ETGASPTSWATRANTAEERHRGDLINKLYLPSGRVDMRQIERTQYLIGSGMDPR	221	Db	164	VRDETGAQSPSWATRANTAEERHRGDLINKLYLPSGRVDMRQIERTQYLIGSGMDPR
Qy	184	SPYLGFIYTSFQERATFISHGNTARQAKERDILQACIGCTTADEKRHETAYKIVEKL	243	Qy	181	TENSPYLGFIYTSFQERATFISHGNTARQAKERDILQACIGCTTADEKRHETAYKIVEKL
Db	222	NPYLGFIYTSFQERATFISHGNTARQAKERDILQACIGCTTADEKRHETAYKIVEKL	281	Db	224	TENSPYLGFIYTSFQERATFISHGNTARLAKGHGDMKLAQICGMIADEKRHETAYKIVEKL
Qy	244	FEIDPDGTVALAFADMMRKKTSMPAHLMYGRDDNLFDHFSAVAQRLGVYTAKYADILEF	303			

Qy	241	EKLFEILDPTCVLAFADMMRKKISMPAHMLYGRDDNLFDHFSAVAQRLGVYTAKDYADI	300	Db	162	ETGASPTPWAUTRATAENRHGDLNLKYLYLSGRVDMRQIEKTIQYLIGSGMDPR TEN 221
Db	284	EKLFEILDPTCVLAFADMMRKKISMPAHMLYGRDDNLFDHFSAVAQRLGVYTAKDYADI	343	Qy	184	SPYLGFTYTSQERATFISHGNTAQRQAKEHGDIKLAQICGTTIAADEKFRHETAYTKIVEKL 243
Qy	301	LEFLVGRWKVDKLGLTGLSABEGQKAODYVCRLLP--RIRRLEERAQRAKEAIPMPESWIE	357	Db	222	NPYLGFTYTSQERATFVSIGNTAQRQAKEHGDIKLAQICGTTIAADEKFRHETAYTKIVEKL 281
Db	344	LEFLVARKVYADLTGSGEGRKAQDYVCRCRPRIRRLEERAQRAKEAIPRLKFSWYI	403	Qy	244	FEIDPDGTVALFADMMRKKISMPAHMLYGRDDNLFDHFSAVAQRLGVYTAKDYADLLEF 303
Qy	358	DROVKL 363		Db	282	LEIDPDGTWYAFADMMRKKISMPAHMLYGRDDNLFDHFSAVAQRLGVYTAKDYADLLEF 341
Db	404	DREVQL 409		Qy	304	LVGRNPKVDTGLSARGQKAODYVCRLLPPIRRLDERAQRCAEATMPWSWIFDROVKL 363
Db	342	LAGRNKIESLSGLSGEGNKAQEYLCLTPRIRRLDERAQRACKGPKIPFSWIDREVQL 401		Db	342	LAGRNKIESLSGLSGEGNKAQEYLCLTPRIRRLDERAQRACKGPKIPFSWIDREVQL 401
RESULT 11						
Q9XQR7		PRELIMINARY:	PRT:	401 AA.	RESULT 12	
ID	Q9XQR7;				065040	PRELIMINARY:
AC					ID	PRT:
DT	01-NOV-1999	(TREMBLref. 12, Created)			065040;	396 AA.
DT	01-NOV-1999	(TREMBLref. 12, Last sequence update)			AC	065040;
DT	01-JUN-2002	(TREMBLref. 21, Last annotation update)			DT	01-AUG-1998 (TREMBLref. 07, Created)
DE		Acyl-lacyl-carrier protein desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).			DT	01-AUG-1998 (TREMBLref. 07, Last sequence update)
DE		(EC 1.14.99.6) (Stearoyl-ACP desaturase).			DT	01-JUN-2002 (TREMBLref. 21, Last annotation update (EC 1.14.99.6) (Stearoyl-ACP desaturase).
GN					DE	
OS					GN	
OG					OS	
OC					RA	
OC		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids III; Brassicales; Brassicaceae; Brassica; Macfadyena.			CAhoon, E.B., Shah, S., Shanklin, J., Browse, J.;	
OC					RT	"Determinant of Substrate Specificity," Predicted from the Acyl-ACP Desaturase of Doxantha Seed.";
OX					RT	Plant Physiol. 0:0-0(1998).
RN	[1]				CC	-!- FUNCTION: Converts Stearoyl-ACP to Oleoyl-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).
RP		SEQUENCE FROM N.A.			CC	-!- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
RC		STRAN=USA JAKISAN;			CC	= OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
RA		Vageshababu H.S., Kirti P.B., Chopra V.L.;			CC	-!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).
RT		"Nucleotide sequence of the coding region of the plastidic delta-9-acyl carrier protein desaturase of Brassica juncea"; Submitted (MAY-1999) to the EMBL/GenBank/DDJU databases.			CC	-!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.
RL					CC	-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC		-!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).			CC	-!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC		-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.			CC	-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
EMBL		EMBL: AF153420; AAD0245.1; -.			DR	EMBL: AF051134; AAC05293.1; -.
DR		HSSP: P2237; IAFR.			DR	InterPro: IPR005067; FA_desat.
DR		InterPro: IPR005067; FA_desat.			DR	InterPro: IPR001225; FA_desat.
DR		Pfam: PF03405; FA_desat.			DR	Pfam: PF03405; FA_desat.
DR		PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.			DR	PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
KW		Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase; Transit peptide.			KW	Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase; Transit peptide.
CC		SEQUENCE 401 AA: 45504 MW: 1722DA429DCFOEB CRC64;			SQ	SEQUENCE 396 AA: 45231 MW: 0101A758556D5C57 CRC64; ;
CC		Query Match 88.5%; Score 1695; DB 8; Length 401;			Qy	1 ASTLKGSKVEENIKKPPMPREHYQVTHSMSPQKIEFKSLDNWAEENLHLKPKVCKWQ 60
CC		Best Local Similarity 86.4%; Pred. No. 1.3e-130; Mismatches 30; Matches 311; Conservative 24; Gaps 0;			Db	34 AATLKGRLDRVEVKTFSPAREHVQVTHSMSPQKIEFKSLDNWAEENLHLKPKVCKWQ 93
DR		4 LKSGSEVENIKKPPMPREHYQVTHSMSPQKIEFKSLDNWAEENLHLKPKVCKWQ 63			Qy	64 CWPQQFLPDPASDGDFEDEVRLRERAKEIIPDDYFVVLGVDMATEALPTYQTMNLNTLDGVD 120
DR		4.2 LSSSTREVEISKKPPKTPKEVHQVQLHSMPQKIEFKSLDNWAEENLHLKPKVCKWQ 101			Db	102 PQDFLDPDPASDGDFEDEVRLRERAKEIIPDDYFVVLGVDMATEALPTYQTMNLNTLDGVD 161
DR		Qy 124 ETGASPTSWAUTRATAENRHGDLNLKYLYLSGRVDMRQIEKTIQYLIGSGMDPR 183			Qy	121 VRDETASPTSWAUTRATAENRHGDLNLKYLYLSGRVDMRQIEKTIQYLIGSGMDPR 180



AC Q42591;  
 DT 01-NOV-1996 (TREMBLref. 01, Created)  
 DT 01-NOV-1996 (TREMBLref. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBLref. 21, Last annotation update)  
 DE Acyl-(acyl-carrier protein) desaturase (EC 1.14.99.6) (Stearoyl-ACP  
 desaturase).  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC eurosids II; Brassicales; Brassicaceae; core eudicots; Rosidae;  
 OC NCBI\_TAXID=3702;  
 OX RN [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-AERIAL PARTS;  
 RA Piffanelli P., Murphy D.J.;  
 RT "Cloning of a stearoyl-ACP desaturase from Arabidopsis thaliana.";  
 RL Submitted (Nov-1995) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Converts stearoyl-ACP to oleoyl-ACP by introduction of a  
 CC C15 double bond between carbons delta-9 and delta-10 of the acyl  
 CC chain (by similarity).  
 CC -!- CATALYTIC ACTIVITY: Stearoyl-(acyl-carrier protein) + AH(2) + O(2)  
 CC = Oleoyl-(acyl-carrier protein) + A + H(2)O.  
 CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY  
 CC SIMILARITY).  
 CC -!- PATHWAY: Catalyzes the principal conversion of saturated fatty  
 CC acids to unsaturated fatty acids in the synthesis of vegetable  
 CC oils.  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
 DR EMBL: X93461; CAA63746.1; -.  
 DR HSSP: P3337; IAPF.  
 DR InterPro: IPR005067; FA\_desat.  
 DR InterPro: IPR012225; FA\_desaturase.  
 DR PFAM: PF03405; FA\_desaturase\_2; 1.  
 DR PROSITE: PS00574; FATTY\_ACID\_DESATUR\_2; 1.  
 KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;  
 KW transpeptidase.  
 SEQUENCE 407 AA; 46102 MW; 823551490844296 CRC64;  
 SQ

Query Match 86.7%; Score 1660.5; DB 10; Length 407;  
 Best Local Similarity 87.9%; Pred. No. 9e-128;  
 Matches 311; Conservative 21; Mismatches 17; Indels 5; Gaps 1;

4 LKSGSKKEVENLKKPMPMPREYHVQVTHSMPPQKIEFLFKSLDNWAEPNVLHLPVKCWW 63  
 Db 42 LSSGPKREVESLKKPMPMPREYHVQVTHSMPPQKIEFLFKSLDNWAEPNVLHLPVKCWW 101  
 Qy 64 PQDFLPPDPSQGDFEDEVYRELERAKETPDYFVVLVGMITEALPYYQTMNLTDGVRD 123  
 Db 102 PQDFLPPDPSQGDFEDEVYRELERAKETPDYFVVLVGMITEALPYYQTMNLTDGVRD 161  
 Qy 124 ETGASPTSWA1WTRATAENRHDGLLNKLYLGSRVDMRQIEKTIQYLGSMDPRTEN 183  
 Db 162 ETGASPTSWA1WTRATAENAHGDLLNKLYLGSRVDMRQIEKTIQYLGSMDPRTEN 221  
 Qy 184 SPYLGFITYTSQERATFISHGNTARQAKEHCDIKLAQICGTTIADEKRHETAYTKEVKL 243  
 Db 222 NPYLGFTYTSQERATFISGNTARQAKEHCDIKLAQICGTTIADEKRHETAYTKEVKL 281  
 Qy 244 FEIDPDGTVALFADMRRKKISMPAHLYMDGRDNLFDFSAVQRLGVYTAKDYADILEF 303  
 Db 282 FEIDPDGTVALFADMRRKKISMPAHLYMDGANDNLFDFNSVSAQRUGVYTAKDYADILEF 341  
 Qy 304 LVGRWKVDKLTLGSLASGQKAODYVCRLLPRTIRRLBERAQRAK-----EAPTMP 352  
 Db 342 LVGRWKQDITLGLSGEGNKAQDYLCLGSLAPRKRLDERAQARAKLGQRQRPILP 395

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4 protein - protein search, using sw model						
run on:	March 7, 2003, 03:04:12	Search time	13 Seconds	GenCore version 5.1.3		
(without alignments)			1158.147 Million cell	updates/s		
Title: US-10-017-145-1						
perfect score:	1916	DB	112892	seqs, 41476328 residues	Score:	RAKEAPTMPFSWIFDRQVKL 363
sequence:	1 ASTLKGSKKEVNLLKKPFMP.....	seq	112892	length: 0	Length:	2000000000
scoring table: BLOSUM62						
Gapop	10.0	Gapext	0.5	Number of hits satisfying chosen parameters:		
searched:	112892	length:	0	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.		
total number of hits satisfying chosen parameters:	112892	Database : SwissProt_40;*				
minimum DB seq length: 0	1	Score	1916	Query	Match	Length
maximum DB seq length: 2000000000	2	DB	1764	STAD_RICINUS	396	1
Post-processing: Minimum Match 0%						
Maximum Match 100%						
Listing first 45 summaries						
SUMMARIES						
Result No.	Score	Match Length	DB ID	Description		
1	1916	100.0	STAD_RICCO	P22337	ricinus	
2	1764	92.1	STAD_CUCSA	P32061	cucumis	
3	1752	91.4	STAD_CARTA	P22243	carthamus	
4	1738	90.7	STAD_SOYBN	Q42907	glycine	
5	1724.5	90.0	STAD_SPIOL	P28653	spinacia	
6	1638	88.6	STAD_BRANA	P29108	brassica	
7	1680	87.7	STAS_BRANA	Q01771	brassicae	
8	1662.5	86.8	STAD_ELAGN	Q42448	elaeis	9
9	1655	86.4	STAD_HELAN	Q96556	helianthus	
10	1652	86.2	STAD_SOLCO	Q41319	solanum	
11	1649	86.1	STAD_OLEEU	Q43543	olea	eur
12	1626	84.9	STAD_SOLEU	P46233	solanum	
13	1610.5	84.1	STAD_GOSHI	Q42770	gossypium	
14	1607	83.9	STAD_SIMMONDS	Q01753	simmondsia	
15	1583	82.6	STAD_ORYSA	Q40731	oryza	sa
16	1465	76.5	STAD_LINUS	P32062	linum	us
17	1317	68.7	STAD_CORS	P32063	coriandrum	
18	104.5	5.5	TKT_BUCAI	P57195	buchnera	
19	101.5	5.3	TEGU_HSVEB	P28935	equine	h
20	101	5.3	S3B1_SCHPO	Q1018	schizosac	
21	99.5	5.2	RIR2_ECOLI	P00453	escherichia	
22	98.5	5.1	S3B1_HUMAN	Q75533	homo	sapiens
23	98.5	5.1	S3B1_MOUSE	Q99m93	mus	musculus
24	98.5	5.1	S3B1_XENLA	Q57938	xenopus	
25	97.5	5.1	YBB9_SCHPO	Q60011	schizosac	
26	97	5.1	S3B1_CHLPN	Q92903	chlamydia	
27	97	5.1	RIR2_DROME	P09vn7	drosophila	
28	96.5	5.0	BP28_DROME	P41121	photinus	
29	96	5.0	PNP_PHOLU	P43533	saccharomy	
30	95.5	5.0	ALR2 YEAST	P37427	salmonella	
31	93.5	4.9	32	671	homo	homo sapiens
32	93.5	4.9	YBB9_SCHEU	Q60502	schizosac	
33	92.5	4.8	YBB9_SCHEU	Q10192	alcaligenes	
34	92.5	4.8	YBB9_SCHEU	Q10192	schizosac	

RESULT 1						
STAD_RICCO	STANDARD	PRT	396 AA.	ALIGNMENTS		
ID_STAD_RICCO						
AC P22337; 1						
DT 01-AUG-1991 (Rel. 19, Created)						
DT 01-AUG-1991 (Rel. 19, Last sequence update)						
DT 15-JUN-2002 (Rel. 41, Last annotation update)						
DE Acyl-[acyl]-carrier protein desaturase, chloroplast precursor (EC 1.14.99.6) (Stearoyl-ACP desaturase) (delta(9) stearoyl-acyl carrier protein desaturase).						
DE Ricinus communis (Castor bean).						
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; tracheophyta; spermatophytes; Magnoliophyta; eudicots; Rosidae; euuroids I; Malpighiales; Euphorbiaceae; Ricinus.						
OC NCBI_TaxID:3988;						
OX [1]						
RN RP SEQUENCE FROM N.A.						
RX MEDLINE=91172837; PubMed=2006187;						
RA Shanklin J.; Somerville C.R.;						
RT "Stearoyl-acyl-carrier protein desaturase from higher plants is structurally unrelated to the animal and fungal homologs.";						
RT Proc. Natl. Acad. Sci. U.S.A. 88:2510-2514 (1991).						
RN [2]						
RN SEQUENCE FROM N.A.						
RC TISSUE=Endosperm;						
RA Knutzon D.S.; Scherer D.E.; Schreckengost W.E.;						
RT "Nucleotide sequence of a complementary DNA clone encoding stearoyl-acyl carrier protein desaturase from castor bean, Ricinus communis.";						
RT from castor seed and its relationship to other di-iron proteins.";						
RL Plant Physiol. 96:344-345(1991).						
RN [3]						
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).						
RX MEDLINE=97015109; PubMed=8861937;						
RA Lindqvist Y.; Huang W.; Schneider G.; Shanklin J.;						
RT "Crystal structure of delta(9) stearoyl-acyl carrier protein desaturase from castor seed and its relationship to other di-iron proteins.";						
RL EMBO J. 15:4081-4092 (1996).						
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN.						
CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)						
CC = oleoyl-1-acyl-carrier protein + A + 2 H(2)O.						
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.						
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.						
CC -1- SUBUNIT: HOMODIMER.						
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF NONPHOTOSYNTHETIC TISSUES.						
CC -1- TISSUE SPECIFICITY: HIGHER LEVELS IN DEVELOPING SEEDS THAN IN LEAF AND ROOT TISSUES.						
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.						
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CC [2] SEQUENCE FROM N.A. RN  
CC MEDLINE=91172837; PubMed=2006187;  
CC Shanklin J., Somerville C.;  
CC RA  
CC RT  
CC structurally unrelated to the animal and fungal homologs.";  
DR EMBL: X59857; AAAT4692; 1; ALT\_INIT.  
DR PIR: S16463; ORCSDAD.  
DR PIR: A39170; A39170.  
DR PIR; 1AFR; 15-MAV-97.  
DR InterPro; IPR005067; FA\_desat.  
DR InterPro; IPR001225; FA\_desat.  
DR Pfam; PF03405; FA\_desat; 2; 1.  
DR PROSITE; PS00574; FATTY\_ACID\_DESATUR\_2; 1.  
DR PROSITE; PS00574; FATTY\_ACID\_DESATUR\_2; 1.  
DR Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;  
KW Transit peptide; 3D-structure;  
FT TRANSIT 1 33 CHLOROPLAST (BY SIMILARITY).  
FT CHAIN 34 396 AA; 45371 MW; E50DA725936392AF CRC64;  
SQ SEQUENCE 396 AA; 45371 MW; E50DA725936392AF CRC64;

Query Match 100.0%; Score 1916; DB 1; Length 396;  
Best Local Similarity 100.0%; Pred. No. 2e-14;  
Matches 363; Conservative 0; Mismatches 0; Gaps 0;  
Query 1 ASTLUSGSKEVNLLKKPMPPEVHYQVTHSMPQKIEFKSLDNWAENILVHLKPKVEK 60  
Db 34 ASTLUSGSKEVNLLKKPMPPEVHYQVTHSMPQKIEFKSLDNWAENILVHLKPKVEK 93

QY 61 CROPQDFELPDPSADGFDEQVRLRERAKEIPDPDYFVVLGDMITEALPLTYQTMNLTDG 120  
Db 94 CROPQDFELPDPSADGFDEQVRLRERAKEIPDPDYFVVLGDMITEALPLTYQTMNLTDG 153

QY 121 VRDGETGASPTSWAIWTRAWTAENRHGDLLNKYLGSRVDMRQIEKTIQYLGSGMOP 180  
Db 154 VRIETGASPTSWAIWTRAWTAENRHGDLLNKYLGSRVDMRQIEKTIQYLGSGMOP 213

QY 181 TENSPLYGTTTFSQERATFISHGNTARQAKHGDIKLQAQGTTIAADEKRHETAYTKIV 240  
Db 214 TENSPLYGTTTFSQERATFISHGNTARQAKHGDIKLQAQGTTIAADEKRHETAYTKIV 273

QY 241 EKLFIEIDPDGTVAFADMRKIKISMPAHMMLYQGRDDNFIDHSAVAGRLGTYTAKDYADI 300  
Db 274 EKLFIEIDPDGTVAFADMRKIKISMPAHMMLYQGRDDNFIDHSAVAGRLGTYTAKDYADI 333

QY 301 LIEFLVGRMKVKDQKUTGSLAEGOKAQDYICRLPPRIRLLEERAGRAKBPAPTMFSWIFDQ 360  
Db 334 LIEFLVGRMKVKDQKUTGSLAEGOKAQDYICRLPPRIRLLEERAGRAKBPAPTMFSWIFDQ 393

QY 361 VKL 363  
Db 394 VKL 396

RESULT 2  
STAD\_CUCSA STANDARD; PRT; 396 AA.  
AC P32061; 27, Created)  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DE Acyl-(acyl-carrier protein) desaturase, chloroplast precursor  
OS Cucumis sativus (Cucumber).  
OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;  
OC Caryophyllales; Cucurbitales; Cucurbitaceae; Cucumis.  
NCBI\_TaxID=3639;  
RN [1] SEQUENCE FROM N.A.  
RC TISSUE=Seedling cotyledon;  
RC Shanklin J., Mullins C., Somerville C.R.;  
RA "Sequence of a complementary DNA from *Cucumis sativus* L. encoding the  
RT stearoyl acyl-carrier protein desaturase.";  
RL Plant Physiol. 97:467-468(1991).  
QY 361 VKL 363



Page 4

Db	343	WKESTLTGSGEGNKAQEXLCGLTPRIRRLDEAQARAKKGPKVPSWIHREVQL	398
Proc.	L	Modification of Brassica seed oil by antisense expression of a stearoyl-acyl carrier protein desaturase gene.;	
[2]		Proc. Natl. Acad. Sci. U.S.A. 89:2624-2628(1992).	
RESULT	7		
SEQUENCE FROM N.A.			
SPRIN=cy, Jet neuf; TISSUE=Leaf;			
MEDLINE=97260965; PubMed=9107041;			
Piffarelli P., Ross J.H., Murphy D.J.;			
"Intra- and extracellular lipid composition and associated gene expression patterns during pollen development in <i>Brassica napus</i> .",			
Plant. J. 11:149-162(1997).			
-1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN.			
-1- CATALYTIC ACTIVITY: Stearoyl-[acyl]-carrier protein + AH(2) + O(2) = Oleoyl-[acyl]-carrier protein + A + 2 H(2)O.			
-1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.			
-1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.			
-1- SUBUNIT: HOMODIMER.			
-1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF NONPHOTOSYNTHETIC TISSUES.			
-1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.			
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EMBL: X60978; CAA43294_1; -;			
EMBL: X97325; CAA65990_1; -;			
PIR: S23351; S23351.			
RSSB: P22337; 1AFR.			
InterPro: IPR005067; FA_desat.			
InterPro: IPR001225; FA_desaturase.			
Pfam: PF03405; FA_desaturase_2; 1.			
PROSITE: PS00574; FATTY ACID DESATUR_2; 1.			
Oxidoreductase; Fatty acid biosynthes; NADP; Chloroplast; transit peptide.			
TRANSIT 1 34 CHLOROPLAST (BY SIMILARITY).			
CHAIN 35 398 AA: 45347 MW: 906898CF41CSF5 CRC64;			
SEQUENCE 398 AA: 45347 MW: 906898CF41CSF5 CRC64;			
Query Match 88.6%; Score: 1658; DB: 1; Length: 398;			
Best Local Similarity 68.2%; Pred. No. 1.3e-123; Mismatches 27; Indels 0; Gaps 0;			
Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;			
Y 8 SKEVENLKKPFMPPREHVQVTHSMPPKIEFKSLDNWAEENILVHLKPVEKCWQPODF 67			
Y 43 SKEVESLKKPFMPPREHVQVTHSMPPKIEFKSLDNWAEENILVHLKPVEKCWQPODF 102			
b 68 LPDASDGDEQVRLERKAEIPDDYFVLYGDMITEQVQLKQVDEQNLTKDVGVRDEQNL 127			
b 103 LPDASDGDEQVRLERKAEIPDDYFVLYGDMITEQVQLKQVDEQNLTKDVGVRDEQNL 162			
b 128 SPTSWAINTRATAEENRGDLNLKYLVLIGSGMDPTTENSYL 187			
b 163 SPTSWAINTRATAEENRGDLNLKYLVLIGSGMDPTTENSYL 222			
b 188 GFIVTSQFRATLSHGNTARQAKERGDKIKAQICGTTIAADERHETATYK1VEKLFED 247			
b 223 GFIVTSQFRATLSHGNTARQAKERGDKIKAQICGTTIAADERHETATYK1VEKLFED 282			
b 248 PDGTIVLAFADMMRKKTISMPAHLMYDGRDNLDFHESAYAQRLGVGTTAKYDADILEFLYGR 307			
b 283 PDGTIVMFAADMMRKKTISMPAHLMYDGRDNLDFHESAYAQRLGVGTTAKYDADILEFLYGR 342			
b 308 WKVKVLTGSAEFGKAQWVCRPRIRLEERQAGRAKEAPTMPSWMDRQVKL 363			
Y 8 SKEVENLKKPFMPPREHVQVTHSMPPKIEFKSLDNWAEENILVHLKPVEKCWQPODF 67			
Y 44 SKEVSSLKKPFMPPREHVQVTHSMPPKIEFKSMEDRAEQNLPLKDVKEWKQPODF 103			
Query Match 87.7%; Score: 1680; DB: 1; Length: 399;			
Best Local Similarity 87.1%; Pred. No. 3.1e-22; Indels 0; Gaps Matches 310; Conservative 29; Mismatches 17;			
Qy 8 SKEVENLKKPFMPPREHVQVTHSMPPKIEFKSLDNWAEENILVHLKPVEKCWQPODF 67			
Db 44 SKEVSSLKKPFMPPREHVQVTHSMPPKIEFKSMEDRAEQNLPLKDVKEWKQPODF 103			
Qy 68 LPDPASDGDEQVRLERKAEIPDDYFVLYGDMITEQVQLKQVDEQNLTKDVGVRDEQNL 127			

Db	104	LFDPAISDFEEDQVKELRERARELPDDYFVYLVGDMTEELALPTYQTMNLTGVRDETGA	163	SQ	SEQUENCE	393 AA;	44857 MW;	C6A8788B8D8A0CC CRC64;
Qy	128	SPTSWA1WTRAWTAEENRHGDLLNKLYLSSGRVMDPRTENSPYL	187	Query Match	86.8%	Score 1662.5;	DB 1;	Length 393;
Db	164	SPTSWA1WTRAWTAEENRHGDLLNKLYLSSGRVMDPRTENNNPYL	223	Best Local Similarity	85.7%	Pred. No. 6.7e-121;		
Qy	188	GFIYTSFQERATEFISHGNTAARQAKEHGDIIKLAQICSTIAADEKRHETAYT1KIVEKLFIED	247	Matches	311;	Conservative	29;	Mismatches 22;
Db	224	GFIYTSFQERATEFISHGNTAARQAKEHGDIIKLAQICSTIAADEKRHETAYT1KIVEKLFIED	283	Qy	1	ASTLKGSKKEVENLKKPMPREHYQVTHSMPPQKIEIIFKSLDNWAENTLVHKPVEK	60	Gaps 1;
Db	248	PGTVLAFADMRKKLISMPAHLMYDGRDDNLDFHESAVAQRLGVYTAKYDADILEFLYGR	307	Db	247	CWQPOQELPDPASDGDFEQVREPAKEIPDDYFVVLGDMITEEALPYQTMNLTG	120	
Qy	284	PGTVLAFADMRKKLISMPAHLMYDGRDDNLDFHESAVAQRLGVYTAKYDADILEFLAGR	343	Qy	1	CWQPOQELPDPASDGDFEQVREPAKEIPDDYFVVLGDMITEEALPYQTMNLTG	150	
Qy	308	WKVDKLTGLSAEGQAKDYYCVRCLPPIRRLBRAQGRAKEAPTMPSWIDRQVKL	363	Db	283	121 VRDETGASPTSWA1WTRAWTAEENRHGDLLNKLYLSSGRVMDPRTENNNPYL	180	
Db	344	WRIESTLGTGSGEENKAQEYLCLGTPPIRRLBRAQRAKKGKIPFSWIDRQVL	399	Qy	1	121 VRDETGASPTSWA1WTRAWTAEENRHGDLLNKLYLSSGRVMDPRTENNNPYL	210	
RESULT 8				Db	151	151 VRDETGASPTSWA1WTRAWTAEENRHGDLLNKLYLSSGRVMDPRTENNNPYL	240	
STAD_ELAGV		STANDARD;	PRT;	Db	211	151 TENSPYLGFIYTSFQERATEFISHGNTAARQAKEHGDIIKLAQICSTIAADEKRHETAYT1KIV	270	
TD	STAD_ELAGV	STANDARD;	PRT;	Db	211	151 TENSPYLGFIYTSFQERATEFISHGNTAARQAKEHGDIIKLAQICSTIAADEKRHETAYT1KIV	270	
AC	O24478;			Qy	241	151 EKLFIELDPDGTIVLAFAADMRRKKISMPAHLMYDGRDDNLDFHESAVAQRLGVYTAKYDADI	300	
DT	15-DEC-1998	(Rel. 37, Created)		Qy	241	151 EKLFIELDPDGTIVLAFAADMRRKKISMPAHLMYDGRDDNLDFHESAVAQRLGVYTAKYDADI	300	
DT	15-DEC-1998	(Rel. 37, Last sequence update)		Db	271	151 EKLFIELDPDGTIVLSFADMKKKISMPAHLMYDGRDDNLDFHESAVAQRLGVYTAKYDADI	330	
DT	15-JUN-2002	(Rel. 41, Last annotation update)		Qy	301	151 LEFLVGRWKVDKLTLGTLSEAGQQAQDVFVCRLPPIRRLBRAQGRAKEAPTMPSWIDRQ	360	
DE	Acyl - lacyl - carrier protein	desaturase, chloroplast precursor		Db	331	151 LEFLINRWKVKGELTGFSGEGRKAQDFVFCTLAPRIRRIERQAERANKQAPRIPCSW1YGRE	390	
DE	Elaeis quinquefolia var. tenera (Oil palm)			Qy	361	151 VKL 363		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			Db	391	151 VQL 393		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Arecoidae;							
OC	Cocaeae; Elaeididae; Elaeis;							
OX								
RN	[1]							
RP	SEQUENCE FROM N. A.							
RC	TISSUE=Mesocarp;							
RA	"Nucleotide sequence of a cDNA clone encoding stearoyl-acyl-carrier-							
RT	protein from Elaeis guineensis var tenera.";							
RL	(In) Plant Gene Register Pgrs6-110.							
CC	-I- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A							
CC	CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL							
CC	CHAIN.							
CC	-I- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)							
CC	= oleoyl-[acyl-carrier protein] + A + 2 H(2)O.							
CC	-I- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.							
CC	-I- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY							
CC	ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE							
CC	OILS.							
CC	-I- SUBUNIT: HOMODIMER (BY SIMILARITY).							
CC	-I- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF							
CC	NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).							
CC	-I- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.							
CC	-----							
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).							
CC	-----							
DR	EMBL; U68756; AAB41041.1; ALT_INIT.							
DR	HSSP; P22337; IAFER.							
DR	InterPro; IPR005067; FA_desat.							
DR	InterPro; IPR01222; FA_desaturase.							
DR	Pfam; PF03405; FA_desaturase_2; 1.							
DR	PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.							
KW	Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;							
PT	TRANSIT peptide	1	31					
PT	TRANSIT	32	393					
CC	CHLOROPLAST (BY SIMILARITY)							
CC	ACYL-[ACYL-CARRIER PROTEIN]							
CC	-----							
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CC	use by non-profit institutions as long as its content is in no way							

RESULT 10						
STAD_SOLOCO	STAD_SOLOCO	STANDARD;	PRT;	393 AA.	SEQUENCE FROM N.A.	TISSUE=Leaf;
Q41319;	AC	37, Created				TRUCCINI M., GRILLIO S., COSTA A., LEONE A.;
15-DEC-1998	DT	37, Last sequence update)				Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
15-DEC-1998	DT					-i- FUNCTION: CONVERTS STEAROYL-ACP TO OLIGO-L-ACP BY INTRODUCTION OF A
15-JUN-2002	DT					CCS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
DE	DE					CHAIN.
EC 1.14 .39.6	DE					-i- CATALYTIC ACTIVITY: Stearoyl (acyl-carrier protein + A + 2 H)2/10.
Solanum commersonii (Commerson's wild potato).	OS					-i- Oleyoyl (acyl-carrier protein + A + 2 H)2/10.
Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;	KW					CC
Transit Peptide.	FT	33	CHLOROPLAST (BY SIMILARITY).			CC
TRANSIT	FT	396	ACYL-(ACYL-CARRIER PROTEIN) DESATURASE.			CC
CHAIN	FT	45078 MW;	97E455A116791B81 CRC64;			CC
SEQUENCE	SQ	396 AA;				CC
Query Match		86.48;	Score 1655;	DB 1;	Length 396;	
Best Local Similarity		86.55;	Pred No. 2, 6<120;			
Matches 314;	Conservative	19;	Mismatches 30;	Indels 0;	Gaps 0;	
QY	1	ASTLKGSKVEYNLKKPMPREHVHQVTHSMPPQKLEIFKSLDNWAEENILVHLKPKVEK	60			
Db	34	ASTIGSATTAVESTKTPPTPMPREHVQVLSHMPPKTEIFKSMEGNAEENILVHLKPKVEK	93			
QY	61	CWQDPDFLPDASDGEQPRERAKEIPDDYFVVLGDMITEALPTYQTMNLNTLG	120			
Db	94	CWQDPDFLPDASDGFMEQVEELRRAKEIPDDYFVVLGDMITEALPTYQTMNLNTLG	153			
QY	121	VRDETGASPTSWATWTRAWTAENRGDLANKYLSSGRDVMRQIEKTTIQYLIGSGMDPR	180			
Db	154	VRDEGATLLGLVWTRAWTAENRGDLAHQYLSSGRDVRQIQTIQYLIGSGMDPR	213			
QY	181	TENSPYLGFIYTSQERATFISHGNTPARQAKEHGDIKLQAQCTGTAADEKRHETAYTKV	240			
Db	214	TENSPYLGFIYTSQERATFISHGNTPARHAKAEHGDVYKLAQMGTLIAADEKRHETAYTKV	273			
QY	241	EKLFEDPDGTYLAFADMMRKTSMPAHLYMDGRDDNLDFHESAVAQRLGVYTAKDYAD	300			
Db	274	EKLFEDPDGTYLAFADMMRKTSMPAHLYMDGRDDNLFENNSAVAQRLGVYTAKDYAD	333			
QY	301	LEFLYGRWKVDKLTLGSAEGQKAQDYVCRPPRIRLLERAQGRAKEAPTMPPSWIFDQ	360			
Db	334	LEFLYGRWKVADLTGLESGERKAQDYVCRPPRIRLLERAQGRAKEAPTMPPSWIFDQ	393			
QY	361	VKL 363				
Db	394	VKL 396				

RESULT 12  
 SEQUENCE FROM N.A.  
 STRAIN=CV. Leccino; TISSUE=Mesocarp;  
 RA Baldoni L., Abbott A.G.;  
 RT "Nucleotide sequence of a cDNA clone from *Olea europaea* encoding a  
 stearoyl-acyl carrier protein desaturase.";  
 RL (In) Plant Gene register PGR96-052.  
 -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A  
 CTC DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL  
 CHAIN.  
 CC CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)  
 CC -> Oleoyl-[acyl-carrier protein] + A + 2 H(2)O.  
 CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.  
 CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY  
 ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE  
 OILS.  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF  
 NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
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 or send an email to license@isb-sib.ch).  
 CC DR EMBL: U58141; ARB67840.1; -  
 DR HSSP: P22337; IAFR.  
 DR InterPro: IPR005067; FA\_desat.  
 DR InterPro: IPR01225; FA\_desaturase.  
 DR PROSITE: PS00574; FATTY\_ACID\_DESATURASE\_2; 1.  
 KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;  
 KW Transit peptide.  
 FT TRANSIT 1 27 CHLOROPLAST (BY SIMILARITY). DESATURASE.  
 FT CHAIN 28 390 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.  
 FT SEQUENCE 390 AA: 44596 MW: 39090432BAC2B3 CRC64;  
 SQ

Query Match 86.1%; Score 1649; DB 1; Length 390;  
 Best Local Similarity 85.1%; Pred. No. 7..3e-120;  
 Matches 309; Conservative 24; Mismatches 30; Indels 0; Gaps 0;

Qy 1 ASTLKSSEKVENLKKPFMPPEVHQVTHSPQKIEFKSLDNWAENILVHLKPEVK 60  
 DB 28 ASTHISPSMVEGVKKPFPPEVHQVTHSPQKIEFNSNNWAQENILVHLKDVK 87  
 Qy 61 CWPQDFELPDPSADGFDEVREERERAKEIIPDDYFVVLGDNITEALPVTQMLNTLDG 120  
 DB 88 CWPQSDLPDSSEGFBQVMEFLRKKEPFDYFVVLGDNITEALPVTQMLNTLDG 147

Qy 121 VRDETGAESPWSAIIWTRAWTAENRHGDLLNKYLSSGRVDMRQTEKTIQYLGSGMDPR 180  
 DB 148 VRDETGAESLTPWAIIWTRAWTAENRHGDLLNKYLSSGRVDMRQTEKTIQYLGSGMDPR 207

Qy 181 TENSPLYGLFITYSFOERATEFISHGNTAARQKEHGDTKLАОIQTGTTIAADEKRHETAYTKIV 240  
 DB 208 TEINNPYGLFITYSFOERATEFISHGNTAARQKEHGDTKLАОIQTGTTIAADEKRHETAYTKIV 267

Qy 241 EKLFELIDPDGTYLAFADMMRKTSMPAHMMDYGRDNLFDEHSAVQLRGVYTAKDYADI 300  
 DB 268 EKLFELIDPDGTYLALDMRKTSMPAHMMDYGRDNLFDEHSAVQLRGVYTAKDYADI 327

Qy 301 LEFLVGRMKVDSLTKLGSBQKAQDQYVCRLLPPIRRLBEGRAKEAFTMPFSWIDRQ 360  
 DB 328 LEFLVGRMDIEKLTKLGSSEGFRKQDQYVCTLPIRRLEAQSRRVKASATBPSWIFGRE 387

Qy 361 VKL 363

STAD\_SOLTU STANDARD: PRT: 393 AA.  
 ID STAD\_SOLTU ID  
 AC P46253;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE ACY-1 [acyl-carrier protein] desaturase, chloroplast precursor  
 DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TAXID=113;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Taylor M.A., Smith S.B., Davies H.V., Burch L.R.;  
 RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.  
 -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A  
 CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL  
 CHAIN.  
 CC -!- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)  
 CC -> oleoyl-[acyl-carrier protein] + A + 2 H(2)O.  
 CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.  
 CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY  
 ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE  
 OILS.  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF  
 NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.  
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 or send an email to license@isb-sib.ch).  
 CC DR EMBL: M91238; AAA3839.1; -.  
 DR HSSP: P22337; IAFR.  
 DR InterPro: IPR005067; FA\_desat.  
 DR InterPro: IPR001225; FA\_desaturase.  
 DR PROSITE: PS00574; FATTY\_ACID\_DESATURASE\_2; 1.  
 DR PROSITE: PS00574; FATTY\_ACID\_DESATURASE\_2; 1.  
 DR KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;  
 KW Transit peptide.  
 FT TRANSIT 1 30 CHLOROPLAST (BY SIMILARITY). ACYL [ACYL CARRIER PROTEIN] DESATURASE.  
 FT CHAIN 31 393 MW: 3933 AA; 44538 MW;  
 SQ

Query Match 84.9%; Score 1626; DB 1; Length 393;  
 Best Local Similarity 82.4%; Pred. No. 4..4e-118;  
 Matches 299; Conservative 34; Mismatches 30; Indels 0; Gaps 0;

Qy 1 ASTLKSSEKVENLKKPFMPPEVHQVTHSPQKIEFKSLDNWAENILVHLKPEVK 60  
 DB 31 ASTHISPSMVEGVKKPFPPEVHQVTHSPQKIEFNSNNWAQENILVHLKDVK 90  
 Qy 61 CWPQDFELPDPSADGFDEVREERERAKEIIPDDYFVVLGDNITEALPVTQMLNTLDG 120  
 DB 91 CWPQDFELPDPSADGFDEVREERERAKEIIPDDYFVVLGDNITEALPVTQMLNTLDG 150

Qy 121 VRDETGAESPWSAIIWTRAWTAENRHGDLLNKYLSSGRVDMRQTEKTIQYLGSGMDPR 180  
 DB 148 VRDETGAESLTPWAIIWTRAWTAENRHGDLLNKYLSSGRVDMRQTEKTIQYLGSGMDPR 207

Qy 181 TENSPLYGLFITYSFOERATEFISHGNTAARQKEHGDTKLАОIQTGTTIAADEKRHETAYTKIV 240  
 DB 208 TEINNPYGLFITYSFOERATEFISHGNTAARQKEHGDTKLАОIQTGTTIAADEKRHETAYTKIV 267

Qy 241 EKLFELIDPDGTYLAFADMMRKTSMPAHMMDYGRDNLFDEHSAVQLRGVYTAKDYADI 300  
 DB 268 EKLFELIDPDGTYLALDMRKTSMPAHMMDYGRDNLFDEHSAVQLRGVYTAKDYADI 327

Qy 301 LEFLVGRMKVDSLTKLGSBQKAQDQYVCRLLPPIRRLBEGRAKEAFTMPFSWIDRQ 360  
 DB 328 LEFLVGRMDIEKLTKLGSSEGFRKQDQYVCTLPIRRLEAQSRRVKASATBPSWIFGRE 387

Qy 361 VKL 363



DR EMBL; MB3199; AAA33932.1; -.

DR InterPro; P22337; IAPR.

DR InterPro; IPR00567; FA\_desat.

DR InterPro; IPR00125; FA\_desaturase.

DR Pfam; PF03405; FA\_desaturase\_2; 1.

DR PROSITE; PS00574; Fatty\_acid\_DESATUR\_2; 1.

KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;

KW Transit peptide.

FT TRANSIT 1 34 CHLOROPAST (BY SIMILARITY)

FT CHAIN 35 398 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.

SEQUENCE 398 AA: 45130 MW; F3E00BB04427DB CRC64;

Query Match Score 1607; DB 1; Length 398;

Best Local Similarity 83.9%; Pred. No. 1; 3e-16;

Matches 287; Conservative 33; Mismatches 33; Indels 0; Gaps 0;

QY 1 ASTLKGSKKEVENLKKPQQKTEIFKSLDNVAEENLVLHLPKEK 60

Db 36 SSMGITSKEIPNAKKHMPREAHQVTKHSPQQKTEIFKSLDNVAEENLVLHLPKEK 95

QY 61 CNOPODFLPDPASDGFDEQVRLERAKEIIPDDYFVVLVGDMDITEEALPYYCOTMLNTLDG 120

Db 96 CNOPODFLPDPASGEMQVKEERKPEIPDDYFVVLVGDMDITEEALPYYCOTMLNTLDG 155

QY 121 VDETGTASPTSAIWIWTRAWTAENRHGDLLNRYYLSGRVMDMROIETKIQVLLIGSGMDPR 180

Db 156 VDETGTASLTSAIWIWTRAWTAENRHGDLLNRYYLGTGRVDKQIETKIQVLLIGSGMDPR 215

QY 181 TENSPLYGLFIYTSQERATFISHGNTARQAKHGDIKLQAQIGTIAADEKRHETAYTKIV 240

Db 216 SENNNPVLGFIYTSQERATFISHGNTARLAKHGDQLQAVQVGTIAADEKRHETAYTKIV 275

QY 241 EKLEFEIDDPGTVLAFADMMRKTSMPAHMLYQGRDDNLFDHSSAVAGRLGYYTAKYADI 300

Db 276 EKLEFEIDDPGAVLALADMMRKTSMPAHMLYQGRDDNLFDHSSAVAGLQVYQIGTYTAKYADI 335

QY 301 LEFLVGRMKVKDILTGSAEKGQYVCRPLPIRRLEERAQRAKEAPTMPSWIFDRO 360

Db 336 LEHLVNRKRVENGLMSGEGHIAQDFVCGLAPRKUGERAQSLSPVSLVPSWIFNKE 395

QY 361 VKL 363

Db 396 LKV 398

RESULT 15

STAD ORYSA STANDARD; PRTR; 390 AA.

ID STAD\_ORYSA STANDARD; PRTR; 390 AA.

AC 31

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor (EC 1.14.99.6) (Stearoyl-ACP desaturase).

OS Oryza sativa (Rice).

OC Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Ehrhartoideae; Oryzeae; Oryza.

OC NCBI\_TAXID=4530; [1]

RN SEQUENCE FROM N\_A.

RC STRAIN=cv. Nipponbare; TISSUE=Seed; MEDLINE=95334510; PubMed=7610181;

RX "Nucleotide sequence of a stearoyl-acyl carrier protein desaturase cDNA from developing seeds of rice."; Plant Physiol. 108:845-846 (1995).

RC -!- FUNCTION: Converts Stearoyl-ACP to Oleoyl-ACP by introduction of a cis double bond between carbons delta-9 and delta-10 of the acyl chain.

CC -!- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2) = oleoyl-[acyl-carrier protein] + A + 2 H<sub>2</sub>O.

CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.

CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.

CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

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CC DR D38752; BAA07631.1; -.

CC DR IHSPP; P22337; IAPR.

CC DR InterPro; IPR005067; FA\_desat.

CC DR InterPro; IPR01225; FA\_desaturase.

CC DR Pfam; PF03405; FA\_desaturase\_2; 1.

CC DR PROSITE; PS00574; FATTY\_ACID\_DESATUR\_2; 1.

CC DR PROSITE; PS00574; ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.

CC KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast.

CC KW Transit peptide.

CC FT CHAIN 1 31 CHLOROPLAST (BY SIMILARITY).

CC FT CHAIN 32 390 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.

CC SQ SEQUENCE 390 AA; 44482 MW; BD974EAC1E85597 CRC04;

Query Match Score 1583; DB 1; Length 390;

Best Local Similarity 81.0%; Pred. No. 8.9e-115;

Matches 294; Conservative 35; Mismatches 30; Indels 4; Gaps 1;

QY 1 ASTLKGSKKEVENLKKPQQKTEIFKSLDNVAEENLVLHLPKEK 60

Db 32 ASTLKGSKKEVENLKKPQQKTEIFKSLDNVAEENLVLHLPKEK 87

QY 61 CNOPODFLPDPASDGFDEQVRLERAKEIIPDDYFVVLVGDMDITEEALPYYCOTMLNTLDG 120

Db 88 SNOQDFLPDPSSDGFDEVKELERAKEIIPDDYFVVLVGDMDVTEEALPYYCOTMLNTLDG 147

QY 121 VDETGTASPTSWAIWTRAWTAENRHGDLLNRYYLSGRVMDMROIETKIQVLLIGSGMDPR 180

Db 148 VDETGTASPTWAWTRAWTAENRHGDLLNRYYLSGRVMDMROIETKIQVLLIGSGMDPR 207

QY 161 TEUSPYLGFITYTSQERATFISHGNTARQAKHGDIKLQAQIGTIAADEKRHETAYTKIV 240

Db 208 TEINNPYLGFLYTSQERATFISHGNTARHAKYDKEVGDLLKQICCTIAADEKRHETAYTKIV 267

QY 241 EKLEFEIDDPGTVLAFADMMRKTSMPAHMLYQGRDDNLFDHSSAVAGRLGYYTAKYADI 300

Db 268 EKLEFEIDDPGTVLAFADMMRKTSMPAHMLYQGRDDNLFDHSSAVAGRLGYYTAKYADI 327

QY 301 LEFLVGRMKVKDILTGSAEKGQYVCRPLPIRRLEERAQRAKEAPTMPSWIFDRO 360

Db 328 LEFLVGRMKVKDILTGSAEKGQYVCRPLPIRRLEERAQRAKEAPTMPSWIFDRO 360

QY 361 VKL 363

Db 388 VKL 390

Search completed: March 7, 2003, 03:09:10

Job time : 15 secs

GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: March 7, 2003, 03:07:27 ; Search time 22 Seconds  
(without alignments)  
1586.218 Million cell updates/sec

Title: US-1.0-017-145-1  
Perfect score: 1916  
Sequence: 1 ASTLKGSKKEVNLKKPFMP.....RAKEAPTMPFSWIFDRQVKL 363

Scoring table: BLOSUM62  
Gapp 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR:73:  
1: Pir1,\*  
2: Pir2,\*  
3: Pir3,\*  
4: Pir4,\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1916	100.0	396	1 OHCSAD	acyl-acyl-carrier
2	1760	91.9	396	2 B39173	acyl-acyl-carrier
3	1752	91.4	396	1 A39173	acyl [acyl-carrier]
4	1738	90.7	411	2 T07806	acyl-acyl-carrier
5	1733	90.4	401	2 E84869	stearoyl-ACP desat
6	1727	90.1	396	2 T14264	acyl [acyl-carrier]
7	1724.5	90.0	399	1 OHSPAD	acyl-acyl-carrier
8	88.8	88.8	396	2 T14268	acyl-acyl-carrier
9	1698	88.6	398	2 S23351	acyl [acyl-carrier]
10	1680	87.7	399	2 S24995	acyl-acyl-carrier
11	1660.5	86.7	407	2 S71264	acyl-acyl-carrier
12	1655	86.4	396	2 T14172	acyl [acyl-carrier]
13	1652	86.2	393	2 S44202	acyl-acyl-carrier
14	1626	84.9	393	2 T07653	acyl-acyl-carrier
15	1610.5	84.1	397	2 T10793	acyl [acyl-carrier]
16	1583	82.6	390	2 T04097	acyl-acyl-carrier
17	1526.5	79.7	394	2 T51494	stearoyl-acyl Carr
18	1465	76.5	396	2 S31959	acyl [acyl-carrier]
19	1358	70.9	401	2 T51493	stearoyl-acyl Carr
20	1318	68.8	374	2 A96502	probable acyl-acyl
21	1317	68.7	385	2 A47245	acyl [acyl-carrier]
22	307	16.0	328	2 T35035	probable acyl-acyl
23	272	14.2	338	2 H70810	probable desal pro
24	267	13.9	338	2 D87182	acyl-ACP desat
25	158	8.2	275	2 C87153	acyl-ACP desat
26	138	7.2	275	2 D70896	probable desA pro
27	112.5	5.9	389	2 D82223	ribonucleoside-dip
28	112.5	5.9	1155	2 G87477	transcription repa
29	108	5.6	744	2 T09541	transketolase (EC

RESULT 1  
OHCSAD  
acyl-acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - castor bean  
N;Alternate names: stearoyl-[acyl-carrier-protein] desaturase  
C;Species: Ricinus communis (castor bean)  
C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 03-Jun-2002  
C;Accession: S16463; A39170  
R;Knutzon, D.S.; Scherer, D.E.; Schreckengost, W.E.  
Plant Physiol. 96, 344-345, 1991  
A;Title: Stearoyl-acyl-carrier protein desaturase from higher plants is structurally  
A;Reference number: S16463  
A;Accession: S16463  
A;Molecule type: mRNA  
A;Residues: 1-396 <KNU>  
A;Cross-references: EMBL:X56508; PMID:921092; PMID:CAA39859.1; PMID:921093  
R;Shanklin, J.; Somerville, C.  
Proc. Natl. Acad. Sci. U.S.A. 88, 2510-2514, 1991  
A;Title: Stearoyl-acyl-carrier protein desaturase from higher plants is structurally  
A;Reference number: A39170  
A;Accession: A39170  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-396 <SHA>  
A;Cross-references: GB:M59858  
A;Note: Parts of this sequence were confirmed by peptide sequencing  
C;Species: Ricinus communis  
C;Family: acyl [acyl-carrier-protein] desaturase  
C;Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase  
F;1-31/Domain: transit peptide (chloroplast) #status predicted <NP>  
F;34-396/Product: acyl-[acyl-carrier-protein] desaturase #status predicted <NP>

## ALIGNMENTS

3.0	105.5	5.5	5.5	2 A75216	hypothetical prote
3.1	105.5	5.5	1490	2 AC3070	DNA (cytosine-5')-
3.2	105	5.5	874	2 F98216	ATP-dependent CLP
3.3	105	5.5	887	2 F98216	endopeptidase CLP
3.4	104.5	5.5	665	2 E84940.	transketolase (EC
3.5	102.5	5.3	1322	2 T24140	hypothetical prote
3.6	102	5.3	3643	2 T36410	probable polyketid
3.7	101.5	5.3	3421	1 WBEB6	367 K tagment prot
3.8	101	5.3	1188	2 T38467	probable nuclear P
3.9	100	5.2	652	2 T20046	hypothetical prote
4.0	99.5	5.2	376	2 RD52R	ribonucleoside-dip
4.1	99.5	5.2	376	2 F91018	ribonucleoside-dip
4.2	99.5	5.2	376	2 H85862	oligoendopeptidase
4.3	98.5	5.1	598	2 D95207	oligoendopeptidase
4.4	98.5	5.1	598	2 D98072	146D nuclear prote
4.5	98.5	5.1	1307	2 T30887	146D nuclear prote

Db	274	EKLEFEIDPDGTIVLAFADMMRKKISMPAHLMYGRDDNLFDHESAYAQRQLGYTTAKDYADI	333	A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-396 <TH0>			
Qy	301	LEFLVGRWKVDKLTLGTLGSAEGOKAQDVCRLPPRIRLERAQRAKEAAPTMPFSWIFDRO	360	A; Cross-references: GB:M61109; NID:9167196; PID:9167197			
Db	334	LEFLVGRWKVDKLTLGTLGSAEGOKAQDVCRLPPRIRLERAQRAKEAAPTMPFSWIFDRO	393	C; Superfamily: acyl-l-acyl-carrier-protein C; Keywords: chloroplast; oxidoreductase			
Qy	361	VKL 363					
Db	394	VKL 396					
<hr/>							
RESULT 2							
B39170		acyl-l-acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - cucumber					
C; Species: <i>Cucumis sativus</i> (cucumber)		C; Accession: B39170		C; Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 03-Jun-2002			
R; Shanklin, J.; Somerville, C.		Proc. Natl. Acad. Sci. U.S.A. 88, 2510-2514, 1991		A; Title: Stearyl-acyl-carrier-protein desaturase from higher plants is structurally un			
A; Reference number: A9170; MUIH:91172837; PMID:2006187		A; Accession: B39170		A; Accession: B39170			
A; Status: preliminary		A; Molecule type: mRNA		A; Status: preliminary			
A; Residues: 1-396 <SHA>		A; Cross-references: GB:M59857		A; Residues: 1-396 <SHA>			
C; Superfamily: acyl-l-acyl-carrier-protein		C; Keywords: chloroplast; oxidoreductase		C; Superfamily: acyl-l-acyl-carrier-protein			
Query Match	91.9%	Score 1760; DB 2; Length 396;		Query Match	91.4%	Score 1752; DB 1; Length 396;	
Best Local Similarity	90.4%	Pred. No. 3_9e-128;		Best Local Similarity	90.1%	Pred. No. 1_6e-124;	
Matches	328;	Conservative 19; Mismatches 16;		Matches	327;	Conservative 18; Mismatches 18;	
Db	34	ASTLGSSSTPKVDNAKKPQQPREVHQVTHSMPQKIEIFKSIEGNAQNLVHLKPEK	93	Db	34	ASTLGSSSTPKVDNAKKPQQPREVHQVTHSMPQKIEIFKSIEGNAQNLVHLKPEK	93
Qy				Qy	1	ASTLKSGSKEVENLKKPMPREPVHQVTHSMPQKIEIFKSIEGNAQNLVHLKPEK	60
Db				Db	94	CWQAOQDFLPDPASDGFQDQVRLERAKEIPIPDYFVVLGDMITEALPTVOTMLNLDG	120
Qy				Qy	61	CWQAOQDFLPDPASDGFQDQVRLERAKEIPIPDYFVVLGDMITEALPTVOTMLNLDG	120
Db				Db	94	CWQAOQDFLPDPASDGFQDQVRLERAKEIPIPDYFVVLGDMITEALPTVOTMLNLDG	153
Qy				Qy	121	VRDETGAPTSWAIWTRAWTAENRHDLLNKYLGLSGRDMRQIEKTIQYLLIGSGMDPR	180
Db				Db	154	VRDETGAPTSWAIWTRAWTAENRHDLLNKYLGLSGRDMRQIEKTIQYLLIGSGMDPR	180
Qy				Qy	181	TENSPYLGFIYTSQERATEFISHGNTARQAKHGDIKLAQICGTTIADEKRHETATKIV	240
Db				Db	214	TENSPYLGFIYTSQERATEFISHGNTARQAKHGDIKLAQICGTTIADEKRHETATKIV	273
Qy				Qy	181	TENSPYLGFIYTSQERATEFISHGNTARQAKHGDIKLAQICGTTIADEKRHETATKIV	240
Db				Db	214	TENSPYLGFIYTSQERATEFISHGNTARQAKHGDIKLAQICGTTIADEKRHETATKIV	273
Qy				Qy	241	EKLFIEIDPDGTIVLAFADMRRKKTISMPAHLMLGDRDNIFDHSAVAGRLGYTTAKDYADI	300
Db				Db	274	EKLFIEIDPDGTIVLAFADMRRKKTISMPAHLMLGDRDNIFDHSAVAGRLGYTTAKDYADI	300
Qy				Qy	301	LEFLVGRWKVDKLTLGTLGSAEGOKAQDVCRLPPRIRLERAKEIPIPDYFVVLGDMITEALPTVOTMLNLDG	333
Db				Db	334	LEFLVGRWKVDAEGLTGLSGEGRKAQDVCGLPPRIRLERAKEIPIPDYFVVLGDMITEALPTVOTMLNLDG	360
Qy				Qy	361	VKL 363	
Db				Db	394	VKL 396	
<hr/>							
RESULT 4							
T07806		acyl-l-acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - soybean					
N; Alternative names: stearoyl-acyl carrier protein desaturase		C; Species: Glycine max (soybean)		C; Accession: T07806			
R; Chen, B.Y.; Janes, H.W.		submitted to the EMBL Data Library, July 1994		R; Chen, B.Y.; Janes, H.W.			
A; Reference number: 216145		A; Accession: T07806		A; Reference number: 216145			
A; Status: preliminary		A; Molecule type: mRNA		A; Status: preliminary			
A; Residues: 1-297		A; Cross-references: EMBL:L31346; NID:9508602; PID:AAA92462.1; PID:9508603		A; Residues: 1-411 <CHE>			
C; Genetics:		C; Genetics:		C; Genetics:			
A; Gene: SACPD		A; Gene: nuclear		A; Gene: nuclear			
C; Superfamily: acyl-l-acyl-carrier-protein] desaturase		C; Superfamily: acyl-l-acyl-carrier-protein] desaturase		C; Superfamily: acyl-l-acyl-carrier-protein] desaturase			
C; Keywords: chloroplast; oxidoreductase		C; Keywords: chloroplast; oxidoreductase		C; Keywords: chloroplast; oxidoreductase			
F; 1-29/Domain: transit peptide (chloroplast) #status predicted <TNP>		F; 1-29/Domain: transit peptide (chloroplast) #status predicted <TNP>		F; 1-29/Domain: transit peptide (chloroplast) #status predicted <TNP>			
Query Match	90.7%	Score 1738; DB 2; Length 411;		Query Match	90.7%	Score 1738; DB 2; Length 411;	
Best Local Similarity	89.4%	Pred. No. 1_9e-123;		Best Local Similarity	89.4%	Pred. No. 1_9e-123;	
Matches	322;	Conservative 25; Mismatches 13;		Matches	322;	Conservative 25; Mismatches 13;	
Db	1	ASTLKSGSKEVENLKKPMPREPVHQVTHSMPQKIEIFKSIEGNAQNLVHLKPEK	60	Db	29	ASTLKSGSKEVENLKKPMPREPVHQVTHSMPQKIEIFKSIEGNAQNLVHLKPEK	88
Qy				Qy	61	CWQAOQDFLPDPASDGFQDQVRLERAKEIPIPDYFVVLGDMITEALPTVOTMLNLDG	120
Db				Db	89	CWQAOQDFLPDPSSSDGFQDQVRLERAKEIPIPDYFVVLGDMITEALPTVOTMLNLDG	148
Qy				Qy			
Db				Db			
<hr/>							
RESULT 3							
A39173		acyl-l-acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - safflower					
C; Species: <i>Carthamus tinctorius</i> (safflower)		C; Accession: A39173		C; Species: <i>Carthamus tinctorius</i> (safflower)			
C; Accession: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002		R; Thompson, G.A.; Scherer, D.E.; Foxall-Van Aken, S.; Kenny, J.W.; Young, H.L.; Shintani		C; Accession: A39173			
A; Title: Primary structures of the precursor and mature forms of stearoyl-acyl carrier		A; Title: Primary structures of the precursor and mature forms of stearoyl-acyl carrier		A; Title: Primary structures of the precursor and mature forms of stearoyl-acyl carrier			
A; Reference number: A39173; MUID:91172850; PMID:2006194		A; Reference number: A39173; MUID:91172850; PMID:2006194		A; Reference number: A39173			
A; Accession: A39173		A; Accession: A39173		A; Accession: A39173			

RESULT 5										
Qy	LEFLVGRWKVEQLTGLSGEGRKAQFYICGLPPRIRLEERAQARYKESSTLKFWSWIHDRE	388	LEFLVGRWKVEQLTGLSGEGRKAQFYICGLPPRIRLEERAQARYKESSTLKFWSWIHDRE	388	LEFLVGRWKVEQLTGLSGEGRKAQFYICGLPPRIRLEERAQARYKESSTLKFWSWIHDRE	388	LEFLVGRWKVEQLTGLSGEGRKAQFYICGLPPRIRLEERAQARYKESSTLKFWSWIHDRE	388	LEFLVGRWKVEQLTGLSGEGRKAQFYICGLPPRIRLEERAQARYKESSTLKFWSWIHDRE	388
Qy	stearoyl-ACP desaturase [imported] - Arabidopsis thaliana		stearoyl-ACP desaturase [imported] - Arabidopsis thaliana		stearoyl-ACP desaturase [imported] - Arabidopsis thaliana		stearoyl-ACP desaturase [imported] - Arabidopsis thaliana		stearoyl-ACP desaturase [imported] - Arabidopsis thaliana	
C;Species:	Arabidopsis thaliana (mouse-ear cress)		Arabidopsis thaliana (mouse-ear cress)		Arabidopsis thaliana (mouse-ear cress)		Arabidopsis thaliana (mouse-ear cress)		Arabidopsis thaliana (mouse-ear cress)	
C;Date:	02-Feb-2001	#sequence_revision	02-Feb-2001	#text_change	16-Feb-2001		02-Feb-2001	#sequence_revision	02-Feb-2001	#text_change
C;Accession:	EF48669		EF48669		EF48669		EF48669		EF48669	
C;Author:	Kauh, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.; Cronin, L.A.; Shen, M.; Vanken, S.E.; Umayam, L.; Tallon, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.		Kauh, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.; Cronin, L.A.; Shen, M.; Vanken, S.E.; Umayam, L.; Tallon, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.		Kauh, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.; Cronin, L.A.; Shen, M.; Vanken, S.E.; Umayam, L.; Tallon, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.		Kauh, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.; Cronin, L.A.; Shen, M.; Vanken, S.E.; Umayam, L.; Tallon, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.		Kauh, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.; Cronin, L.A.; Shen, M.; Vanken, S.E.; Umayam, L.; Tallon, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.	
A;Status:	preliminary		preliminary		preliminary		preliminary		preliminary	
A;Molecule type:	DNA		DNA		DNA		DNA		DNA	
A;Cross-references:	GB:AE002093; PIDN:92281099; PMID:20083487; PMID:10617197		GB:AE002093; PIDN:92281099; PMID:20083487; PMID:10617197		GB:AE002093; PIDN:92281099; PMID:20083487; PMID:10617197		GB:AE002093; PIDN:92281099; PMID:20083487; PMID:10617197		GB:AE002093; PIDN:92281099; PMID:20083487; PMID:10617197	
C;Genetics:										
A;Gene:	At2g43710		At2g43710		At2g43710		At2g43710		At2g43710	
C;Superfamily:	acyl- [acyl-carrier-protein] desaturase		acyl- [acyl-carrier-protein] desaturase		acyl- [acyl-carrier-protein] desaturase		acyl- [acyl-carrier-protein] desaturase		acyl- [acyl-carrier-protein] desaturase	
Query	90 4%; Score 1733; DB 2; Length 401;		90 4%; Score 1733; DB 2; Length 401;		90 4%; Score 1733; DB 2; Length 401;		90 4%; Score 1733; DB 2; Length 401;		90 4%; Score 1733; DB 2; Length 401;	
Best Local Similarity	89 4%; Fred. No. 4		89 4%; Fred. No. 4		89 4%; Fred. No. 4		89 4%; Fred. No. 4		89 4%; Fred. No. 4	
Matches	322; Conservative		22; Mismatches		16; Indels		0; Gaps		0; Gaps	
Qy	4 LKSGSGKEVENLKKPMPPREVHVVQVTHSMPQKIEFLKSDLNWAENLYHLKPVEKCWQ	63	4 LKSGSGKEVENLKKPMPPREVHVVQVTHSMPQKIEFLKSDLNWAENLYHLKPVEKCWQ	63	4 LKSGSGKEVENLKKPMPPREVHVVQVTHSMPQKIEFLKSDLNWAENLYHLKPVEKCWQ	63	4 LKSGSGKEVENLKKPMPPREVHVVQVTHSMPQKIEFLKSDLNWAENLYHLKPVEKCWQ	63	4 LKSGSGKEVENLKKPMPPREVHVVQVTHSMPQKIEFLKSDLNWAENLYHLKPVEKCWQ	63
Db	42 LSSSFKEVESELKKKFTPPREVHVVQVTHSMPQKIEFLKSDLNWAENLYHLKPVEKSWQ	101	42 LSSSFKEVESELKKKFTPPREVHVVQVTHSMPQKIEFLKSDLNWAENLYHLKPVEKSWQ	101	42 LSSSFKEVESELKKKFTPPREVHVVQVTHSMPQKIEFLKSDLNWAENLYHLKPVEKSWQ	101	42 LSSSFKEVESELKKKFTPPREVHVVQVTHSMPQKIEFLKSDLNWAENLYHLKPVEKSWQ	101	42 LSSSFKEVESELKKKFTPPREVHVVQVTHSMPQKIEFLKSDLNWAENLYHLKPVEKSWQ	101
Qy	64 PDDFLPDASDGDFEQQVRELREAKEI PDDFYVFLVGDMMTEEAFLPTYQTMNLNTLDGVRD	123	64 PDDFLPDASDGDFEQQVRELREAKEI PDDFYVFLVGDMMTEEAFLPTYQTMNLNTLDGVRD	123	64 PDDFLPDASDGDFEQQVRELREAKEI PDDFYVFLVGDMMTEEAFLPTYQTMNLNTLDGVRD	123	64 PDDFLPDASDGDFEQQVRELREAKEI PDDFYVFLVGDMMTEEAFLPTYQTMNLNTLDGVRD	123	64 PDDFLPDASDGDFEQQVRELREAKEI PDDFYVFLVGDMMTEEAFLPTYQTMNLNTLDGVRD	123
Db	102 PDDFLPDASDGDFEQQVRELREAKEI PDDFYVFLVGDMMTEEAFLPTYQTMNLNTLDGVRD	161	102 PDDFLPDASDGDFEQQVRELREAKEI PDDFYVFLVGDMMTEEAFLPTYQTMNLNTLDGVRD	161	102 PDDFLPDASDGDFEQQVRELREAKEI PDDFYVFLVGDMMTEEAFLPTYQTMNLNTLDGVRD	161	102 PDDFLPDASDGDFEQQVRELREAKEI PDDFYVFLVGDMMTEEAFLPTYQTMNLNTLDGVRD	161	102 PDDFLPDASDGDFEQQVRELREAKEI PDDFYVFLVGDMMTEEAFLPTYQTMNLNTLDGVRD	161
Qy	124 ETGASPTSAIWTRAWTAEENRHGLLNLKLYLSSGRVDMQIEKTIQYLIGSGMDPRTEN	183	124 ETGASPTSAIWTRAWTAEENRHGLLNLKLYLSSGRVDMQIEKTIQYLIGSGMDPRTEN	183	124 ETGASPTSAIWTRAWTAEENRHGLLNLKLYLSSGRVDMQIEKTIQYLIGSGMDPRTEN	183	124 ETGASPTSAIWTRAWTAEENRHGLLNLKLYLSSGRVDMQIEKTIQYLIGSGMDPRTEN	183	124 ETGASPTSAIWTRAWTAEENRHGLLNLKLYLSSGRVDMQIEKTIQYLIGSGMDPRTEN	183
Db	162 ETGASPTSAIWTRAWTAEENRHGLLNLKLYLSSGRVDMQIEKTIQYLIGSGMDPRTEN	221	162 ETGASPTSAIWTRAWTAEENRHGLLNLKLYLSSGRVDMQIEKTIQYLIGSGMDPRTEN	221	162 ETGASPTSAIWTRAWTAEENRHGLLNLKLYLSSGRVDMQIEKTIQYLIGSGMDPRTEN	221	162 ETGASPTSAIWTRAWTAEENRHGLLNLKLYLSSGRVDMQIEKTIQYLIGSGMDPRTEN	221	162 ETGASPTSAIWTRAWTAEENRHGLLNLKLYLSSGRVDMQIEKTIQYLIGSGMDPRTEN	221
Qy	184 SPYGLFVYIYFSQERATFISGNNTAQAEKHDIKLQICGTIAADEKRPTEKVKL	243	184 SPYGLFVYIYFSQERATFISGNNTAQAEKHDIKLQICGTIAADEKRPTEKVKL	243	184 SPYGLFVYIYFSQERATFISGNNTAQAEKHDIKLQICGTIAADEKRPTEKVKL	243	184 SPYGLFVYIYFSQERATFISGNNTAQAEKHDIKLQICGTIAADEKRPTEKVKL	243	184 SPYGLFVYIYFSQERATFISGNNTAQAEKHDIKLQICGTIAADEKRPTEKVKL	243
Db	222 NPYLGFLFVYIYFSQERATFISGNNTAQAEKHDIKLQICGTIAADEKRPTEKVKL	281	222 NPYLGFLFVYIYFSQERATFISGNNTAQAEKHDIKLQICGTIAADEKRPTEKVKL	281	222 NPYLGFLFVYIYFSQERATFISGNNTAQAEKHDIKLQICGTIAADEKRPTEKVKL	281	222 NPYLGFLFVYIYFSQERATFISGNNTAQAEKHDIKLQICGTIAADEKRPTEKVKL	281	222 NPYLGFLFVYIYFSQERATFISGNNTAQAEKHDIKLQICGTIAADEKRPTEKVKL	281
Qy	244 FEIDPDGTYLAFADMRKIKTSMPAHMLYDGRDDNLDFHFSQAQRLGVYTAKYDADLTF	303	244 FEIDPDGTYLAFADMRKIKTSMPAHMLYDGRDDNLDFHFSQAQRLGVYTAKYDADLTF	303	244 FEIDPDGTYLAFADMRKIKTSMPAHMLYDGRDDNLDFHFSQAQRLGVYTAKYDADLTF	303	244 FEIDPDGTYLAFADMRKIKTSMPAHMLYDGRDDNLDFHFSQAQRLGVYTAKYDADLTF	303	244 FEIDPDGTYLAFADMRKIKTSMPAHMLYDGRDDNLDFHFSQAQRLGVYTAKYDADLTF	303
Db	282 FEIDPDGTYMAFDMRKIKTSMPAHMLYDGRDNFLDFNFSQAQRLGVYTAKYDADLTF	341	282 FEIDPDGTYMAFDMRKIKTSMPAHMLYDGRDNFLDFNFSQAQRLGVYTAKYDADLTF	341	282 FEIDPDGTYMAFDMRKIKTSMPAHMLYDGRDNFLDFNFSQAQRLGVYTAKYDADLTF	341	282 FEIDPDGTYMAFDMRKIKTSMPAHMLYDGRDNFLDFNFSQAQRLGVYTAKYDADLTF	341	282 FEIDPDGTYMAFDMRKIKTSMPAHMLYDGRDNFLDFNFSQAQRLGVYTAKYDADLTF	341
Qy	304 LVGRKVKVDKLTGLSSEQKAQDQYICVRLPPRIRLEERAQGRKEAFTMPMSWIFDQVKL	363	304 LVGRKVKVDKLTGLSSEQKAQDQYICVRLPPRIRLEERAQGRKEAFTMPMSWIFDQVKL	363	304 LVGRKVKVDKLTGLSSEQKAQDQYICVRLPPRIRLEERAQGRKEAFTMPMSWIFDQVKL	363	304 LVGRKVKVDKLTGLSSEQKAQDQYICVRLPPRIRLEERAQGRKEAFTMPMSWIFDQVKL	363	304 LVGRKVKVDKLTGLSSEQKAQDQYICVRLPPRIRLEERAQGRKEAFTMPMSWIFDQVKL	363
Db	342 LVGRKVKQDUTGLSSEGNAQDYLGLAPRKLDERAQAKRGGPKIPFSWIHDREVQL	401	342 LVGRKVKQDUTGLSSEGNAQDYLGLAPRKLDERAQAKRGGPKIPFSWIHDREVQL	401	342 LVGRKVKQDUTGLSSEGNAQDYLGLAPRKLDERAQAKRGGPKIPFSWIHDREVQL	401	342 LVGRKVKQDUTGLSSEGNAQDYLGLAPRKLDERAQAKRGGPKIPFSWIHDREVQL	401	342 LVGRKVKQDUTGLSSEGNAQDYLGLAPRKLDERAQAKRGGPKIPFSWIHDREVQL	401

C;Species: Helianthus annuus (common sunflower)	C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C;Accession: 'T14246	
R;Hongrakul, V.; Slabaugh, M.B.; Knapp, S.J.	
submitted to the EMBL Data Library, February 1997	
A;Description: Sunflower Stearyl-ACP desaturase.	
A;Reference number: T14246	
A;Status: preliminary; translated from GB/EMBL/DBJ	
A;Molecule type: mRNA	
A;Residues: 1-396 <HON>	
A;Cross-references: EMBL:U91339; NID:92290399; PID:92290400	
A;Experimental source: strain Mammoth	
C;Function:	
A;Description: introduces a double bond at the delta(9) position of stearoyl	
C;Superfamily: acyl-[acyl-carrier-protein] desaturase	
C;Keywords: fatty acid biosynthesis; oxidoreductase	
Query Match Score 1727; DB 2; Length 396;	
Best Local Similarity 88.7%; Pred. No. 1.e-122;	
Matches 322; Conservative 23; Mismatches 18; Indels 0; Gaps	
Qy 1 ASTLKGSSKEVENLKKPFMPPREYHVOYTHSMPQKIBFKSLDNWAFENILVHLKPVKE 60	
Db 34 ASTIGSSPKVKESTKKPTEPPREYHVOYTHSMPQKIBFKSTEGWBDNVLVHLKPVKE 93	
Qy 61 CWQOPDFLPDPASDFGDEQVRERAKETPDYFVVLGDMITEALPQTQTMNLNTLDG 120	
Db 94 CWQOPDFLPPEASDFGEEQVKELRARAETKPDYFVVLGDMITEALPQTQTMNLNTLDG 153	
Qy 121 VRDETGAASPSTSWAIWTRAWTAEENRHGDLLNKYLQLSGRVDMDRQIQTQTOYLIGSGMDPR 180	
Db 154 VRDETGAASPPTPWAIWTRAWTAEENRHGDLLHQVYLSGRVDMDRQIQTQTOYLIGSGMDPR 213	
Qy 181 TENSPLYGLIYTSFQERATEFISGNTAQRQAKEHGDIIKLAQICGTTIAADEKRHETAYTKIV 240	
Db 214 EKLEFEIDDPGTVLAFADMRRKKLSPMPAHLYMDGRDDNLFDHFSAVAQRQLGVYTAKDYADI 273	
Qy 241 EKLEFEIDDPGTVLAFADMRRKKLSPMPAHLYMDGRDDNLFDHFSAVAQRQLGVYTAKDYADI 300	
Db 274 EKLEFEIDDPGTVLAFADMRRKKLSPMPAHLYMDGRDDNLFDHFSAVAQRQLGVYTAKDYADI 333	
Qy 301 LEFLVGRMKVDKDLTGLSAEGQKAOQDYVCGRLPPTRRLBERAQGRAKEAFTMPFSWIFDRQ 360	
Db 334 LEFLVGRMKVADLTGLSGEGRKAQDYVGLPSRTRRLERAARAKEGPSIPFSWIFDRQ 393	
Qy 361 VKL 363	
Db 394 VKL 396	
..	
RESULT 7	
OISPAD	
N;Alternative names: stearoyl-l-acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - spinach	
C;Species: Spinacia olaracea (spinach)	
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 03-Jun-2002	
C;Accession: S22410; S18183	
R;Nishida, I.; Beppu, T.; Matsuo, T.; Murata, N.	
Plant Mol. Biol. 19, 711-713, 1992	
A;Title: Nucleotide sequence of a cDNA clone encoding a precursor to stearoyl	
A;Description: Sunflower Stearyl-ACP desaturase.	
A;Reference number: S22480; MUID:92329733; PMID:1627785	
A;Accession: S22480	
A;Molecule type: mRNA	
A;Residues: 1-399 <NTS>	
A;Cross-references: EMBL:X62898; NID:91229; PID:CAA4687_1; PID:921230	
C;Superfamily: acyl-[acyl-carrier-protein] desaturase	
C;Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase	
F;1-359/Domain: transit peptide (chloroplast) #status predicted <TNP>	
F;36-399/Product: acyl-[acyl-carrier-protein] desaturase #status predicted <	
Query Match Score 1724.5; DB 1; Length 399;	
Best Local Similarity 87.9%; Pred. No. 1.0e-122;	



A; Accession: S24995	Qy 244 FEIDPGTVLAFADMMRKKISMPAHLYMDGRDDNLDFHESAVQRLGVYTAKDYADELIEF 303
A; Molecule type: mRNA	A; Residues: 1-199 <SLO>
A; Cross-references: EMBL:X63344; NID:917869; PID:CAA4964.1; PID:917870	A; Cross-references: acyl [acyl]-carrier protein desaturase
C; Superfamily: acyl [acyl]-carrier protein desaturase	C; Superfamily: chloroplast; fatty acid biosynthesis; homodimer; oxidoreductase
C; Keywords: chloroplast; fatty acid biosynthesis; homodimer; oxidoreductase	
Query Match	87.7%; Score 1680; DB 2; Length 399;
Best Local Similarity	87.1%; Pred. No. 4.2e-19;
Matches 310; Conservative 29; Mismatches 17; Indels 0; Gaps 0;	;
RESULT 12	
Qy 8 SKEVENLKKPMPREPVHYQVYTHSMPPKIEFKSLDNNAEENTLVHLKPEVKCWPQDF 67	T14172
Db 44 SKEVESSLKKPMPREPVHYQVYTHSMPPKIEFKSLDNNAEENTLVHLKPEVKCWPQDF 103	acyl-acyl-carrier-protein] desaturase (EC 1.14.19.2) - common sunflower
Db 68 LPDPASDGFEEQVRLERKEIPTDYFVYLVGDMITEELPLPTQTMNLTGVRDTEA 127	N; Alternate names: stearoyl-ACP desaturase
Db 104 LPDPASDGFEDQVKELERRELPLDYFVYLVGDMITEELPLPTQTMNLTGVRDTEA 163	C; Species: <i>Helianthus annuus</i> (common sunflower)
Db 128 SPTSWIAIWTRAWTAEEBNRHDLLNKYVLSGRVDMRQIENTQYLIGSMQDPRNNPVL 187	C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
Db 164 SPTSWIAIWTRAWTAEEBNRHDLLNKYVLSGRVDMRQIENTQYLIGSMQDPRNNPVL 223	R; Coughlan, S.J.; Hastings, C.E.; Winfrey, R.J.
Db 188 GFIYTSFQERATFISHGNTPARQAEKGHDIKLQAOICGTTIAADEKRHETAYTKIVEKLFID 247	submitted to the EMBL Data Library, September 1996
Db 224 GFIYTSFQERATFVSHGNTPARQAEKGHDIKLQACIGTTIAADEKRHETAYTKIVEKLFID 283	A; Description: Sunflower stearoyl-ACP desaturase.
Db 248 PDGTVLAFAFMRMKRKISMPAHLYMDGRDDNLDFHESAVQRLGVYTAKDYADELIEF 307	A; Reference number: Z17901.
Db 284 PDGTVVAFAFMRMKRKISMPAHLYMDGRDDNLDFHESAVQRLGVYTAKDYADELIEF 343	A; Accession: T14172
Db 308 WKVDKLTKLGAEGOKAQADYVCRLPPRIRLEREAQRAKEAPTMPSWIDFQYKVL 363	A; Status: preliminary; translated from GB/EMBL/DDJB
Db 344 WRIESLTGSGEGNKAQAEYLCGLTPRIRRLDERAQARAKGPKIPFSWIHDREVQI 399	A; Molecule type: mRNA
RESULT 13	
* S71264 acyl-acyl-carrier-protein] desaturase (EC 1.14.19.2) - <i>Arabidopsis thaliana</i>	
C; Species: <i>Arabidopsis thaliana</i> (mouse-ear cress)	N; Alternate names: stearoyl-ACP desaturase
C; Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 03-Jun-2002	C; Species: <i>Arabidopsis thaliana</i> (mouse-ear cress)
C; Accession: S71264	C; Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 03-Jun-2002
R; Piffanelli, P.; Murphy, D.J.	C; Description: Cloning of a stearoyl-ACP desaturase from <i>Arabidopsis thaliana</i> .
submitted to the EMBL Data Library, November 1995	A; Reference number: S71264
A; Molecule type: mRNA	A; Accession: S71264
A; Cross-references: EMBL:X93446; NID:91107506; PID:CAA63746.1; PID:91107507	A; Residues: 1-407 <PfP>
C; Superfamily: acyl [acyl]-carrier protein desaturase	C; Superfamily: acyl [acyl]-carrier protein desaturase
C; Keywords: fatty acid biosynthesis; oxidoreductase	C; Keywords: fatty acid biosynthesis; oxidoreductase
Query Match	86.7%; Score 1660.5; DB 2; Length 407;
Best Local Similarity	87.9%; Pred. No. 1.3e-17;
Matches 311; Conservative 21; Mismatches 17; Indels 5; Gaps 1;	;
RESULT 14	
Qy 4 LKSGSKVEENLKKPMPREPVHYQVYTHSMPPKIEFKSLDNNAEENTLVHLKPEVKCWPQDF 63	S4202
Db 42 LSSGPREVESSLKKPPTPPREPVHYQVYTHSMPPKIEFKSLDNNAEENTLVHLKPEVKCWPQDF 101	acyl-acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - Commerson's wild potato
Qy 64 PQDFLPPDPSDGFEDQYRERERAKEIPDDYFVVLGDMTEEAALPLTYQMLNLTGVRD 123	N; Alternate names: stearoyl-ACP desaturase
Db 102 PQDFLPPDPSDGFEDQYRERERAKEIPDDYFVVLGDMTEEAALPLTYQMLNLTGVRD 161	C; Species: <i>Solanum commersonii</i> (Commerson's wild potato)
Qy 124 ETGASPTSWAIWTRAWTAEEENRHDILNKYVLYLSGRVDMRQIEKTIQYLGSQMDPRTEI 183	C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 03-Jun-2002
Db 162 ETGASPTSWAIWTRAWTAEEENRHDILNKYVLYLSGRVDMRQIEKTIQYLGSQMDPRTEI 221	C; Accession: S41202
Qy 184 SPYLGFIYTSQERATFISHGNTARQAEKGDIKLQACICCTIAADEKRHETAYTKIVEKL 243	
Db 222 NPYLGFIYTSQERATFISHGNTARQAEKGDIKLQACICCTIAADEKRHETAYTKIVEKL 281	

R;Trucci, M.; Grillo, S.; Costa, A.; Leone, A. Submitted to the EMBL Data Library, April 1994 A;Reference number: S44202	Qy 1 ASTLKSGSKVEVNLUKPKPMPPREVHQVITHSMPPQKIEFKSLDNWAEEENILVHLKPKVEK 60 Db 31 ASTHRSPEVGSKVKAFTPPREVHQVITHSMPPKIEFKSLRDWAQNLLVHLKPKVEK 90
A;Molecule type: mRNA A;Residues: 1-393 <TRU>	Qy 61 CWOQDFLDPDASGDFEDEVRELREAKEIPDDYFVVLGDMTEEAALPTYQTMNLNTLDG 120 Db 91 CWOQDFLDPDASGDFEDEVKELREKEIPDDYFVVLGDMTEEAALPTYQTMNLNTLDG 150
A;Cross-references: EMBL:X78935; NID:9474832; PIDN:CAA55535.1; PID:9474833 C;Genetics: A;Genome: nuclear C;Superfamily: acyl-[acyl]-carrier protein desaturase C;Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase F;1-30/Domain: transit peptide (chloroplast) #status predicted <TNP> F;31-393/Product: acyl-[acyl]-carrier-protein desaturase #status predicted <MAT>	Qy 61 CWOQDFLDPDASGDFEDEVRELREAKEIPDDYFVVLGDMQIEKTTQYLGSGMDPR 180 Db 151 VDETGAAPTSMALWTRATAEENRGDLNLKLYLSGRVDMQIEKTTQYLGSGMDPR 210
Query Match 86.2%; Score 1652; DB 2; Length 393; Best Local Similarity 84.8%; Pred. No. 5.4e-117; Matches 308; Conservative 24; Mismatches 31; Indels 0; Gaps 0;	Qy 181 TENSPYLGPIYTSQERATFISHGNTAQAKEHGDILQAQICGTTIAADEKRHETAYTKIV 240 Db 211 TENPPIYLGIVYTSURKGCTFVSIGNTARAKENGDMKLAQICGTTIAADEKRHETAYTKIV 270
Qy 1 ASTLKSGSKVEVNLUKPKPMPPREVHQVITHSMPPQKIEFKSLDNWAEEENILVHLKPKVEK 60 Db 31 ASTRPPSYEDGNYKPKPSPPREVHQVITHSMPPKEIREFDSLHGWAENNLGHHLKPKVEK 90	Qy 241 EKLEFIDPDGTVLAFADMWRKKSIMPALMVGDRDDNLFDHFSAVAQRLGVYTTAKDYADI 300 Db 271 EKLEVDPDGAVLAIGDMWRKNSIMPALMVGDRDDNLFEHFSAVAQRLGVYTTAKDYADI 330
Qy 61 CWOQDFLDPDASGDFEDEVRELREAKEIPDDYFVVLGDMTEEAALPTYQTMNLNTLDG 120 Db 91 CWOQDFLDPDASGDFEDEVKELREKEIPDDYFVVLGDMTEEAALPTYQTMNLNTLDG 150	Qy 301 LEFVGRKVKVDKLTGSLSEGOKAQDYVCRLLPPRIRRLERERAGRAKEEPTMPSSWIFPRQ 360 Db 331 LEFHGRNEVEKLTGSLSEGRRQDYVCGLAPRKLEERAQAKHAKSVPSWIFRQE 390
Qy 121 VDETGAAPTSMALWTRATAEENRGDLNLKLYLSGRVDMQIEKTTQYLGSGMDPR 180 Db 151 VDETGAAPTSMALWTRATAEENRGDLNLKLYLSGRVDMQIEKTTQYLGSGMDPR 210	Qy 361 VKL 363 Db 391 IKL 393
Qy 181 TENSPYLGPIYTSQERATFISHGNTAQAKEHGDILQAQICGTTIAADEKRHETAYTKIV 240 Db 211 TENPPIYLGIVYTSURKGCTFVSIGNTARAKENGDMKLAQICGTTIAADEKRHETAYTKIV 270	RESULT 15 T10793 acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - upland cotton N:Alternative names: delta 9 stearoyl-acyl-carrier protein] desaturase C:Species: Gossypium hirsutum (upland cotton) C:Accession: T10793 C:Domain: 16-Jul-1999 #text_change 03-Jun-2002 R:Liu, Q.; Singh, S.; Sharp, P.; Green, A.; Marshall, D.R. Plant Physiol. 110, 1436, 1996 A:Title: Nucleotide sequence of a cDNA from Gossypium hirsutum encoding a stearoyl-acyl-carrier-protein desaturase (EC 1.14.19.2) precursor - upland cotton A:Reference number: 217148 A:Accession: T10793 A:Cross references: ENBL:X5988; NID:91217627 A:Experimental source: cultivar deltapine-16 C:Function: A:Pathway: fatty acid biosynthesis C:Superfamily: acyl-[acyl-carrier-protein] desaturase C:Species: Gossypium hirsutum C:Accession: T10793 C:Domain: 16-Jul-1999 #text_change 03-Jun-2002 R:Taylor, M.A.; Smith, S.B.; Davies, H.V.; Burch, L.R. Submitted to the EMBL Data Library, April 1992 A:Description: The primary structure of a cDNA clone of the stearoyl-acyl carrier protein desaturase (EC 1.14.19.2) precursor - potato A:Accession: T07653 A:Status: preliminary; translated from GB/EMBL/DBJ A:Molecule type: mRNA A;Residues: 1-393 <TRU> A;Cross references: EMBL:M91238; NID:9169564; PIDN:AAA33839.1; PID:9169565 C;Genetics: A;Genome: nuclear C;Function: A:Description: catalyzes the formation of double bonds at the delta(9) position of stearoyl-acyl carrier protein desaturase C;Superfamily: acyl-[acyl]-carrier protein desaturase C;Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase
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Qy 2 STLKSGSKVEVNLUKPKPMPPREVHQVITHSMPPQKIEFKSLDNWAEEENILVHLKPKVEK 61 Db 35 STPGSGKEVGNLKKPPTPKEVQVQTHSMPPKIEFKSLGNENILVHLKPKVEK 94	Qy 122 RDETGAAPTSMALWTRATAEENRGDLNLKLYLSGRVDMQIEKTTQYLGSGMDPR 181 Db 155 RDETGAAPTSMALWTRATAEENRGDLNLKLYLSGRVDMQIEKTTQYLGSGMDPR 214
Qy 182 ENSPYLGPIYTSQERATFISHGNTAQAKEHGDILQAQICGTTIAADEKRHETAYTKIV 241	Qy 182 ENSPYLGPIYTSQERATFISHGNTAQAKEHGDILQAQICGTTIAADEKRHETAYTKIV 241

Db	215	ENSPYRGFIYTFSQERATEFISHGNTGRLAKEYGDINLAQICGSIASDEKKHETAYTKIVE	274
Qy	242	KLFELIDDPGTVLAFADMMRKISMPAHMLYDGRDDNLFDIHSAYAQLGYTTAKDYADIL	301
Db	275	KLFELIDDPGTVLAFADMMKKIAMPAAEFIDGRDNLFDIHSAYAQLGYTTAKDYADIV	334
Qy	302	EFLYGRWKVDKLTGISAEGGKAQDYVCRLPPRIRLEERAQGRAK-EAPTMPEFSWTFDRC	360
Db	335	EHLVDRWKVKELAGLISAEGGKAQDYCSSLSSRIRLEERAQEKAGSPTVSPFSWTFDRC	394
Qy	361	VKL 363	
Db	395	VKL 397	

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Job time : 23 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2003, 03:10:02 : Search time 16 Seconds  
(without alignments)  
956.736 Million cell updates/sec

Title: US-10-017-145-1  
Perfect score: 1916  
Sequence: ASPLKSGSKEVENLKKPFMP . . . . . RAKEAPTMPSWLFDRQVKL 363

Scoring table: BLOSUM62  
Gapext 0.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA: \*

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5: /cgn2_6/podata/1/pubpaas/US07__NEW_PUB.pep:*
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12: /cgn2_6/podata/1/pubpaas/US10__PUBCOMB.pep:*
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14: /cgn2_6/podata/1/pubpaas/US60__PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1916	100.0	363	10 US-09-988-929A-1	Sequence 1, Appli
2	1916	100.0	363	12 US-10-017-145-1	Sequence 1, Appli
3	1637	85.4	396	10 US-09-837-151-2	Sequence 2, Appli
4	291	15.2	54	9 US-09-730-763-12	Sequence 2, Appli
5	286	14.9	54	9 US-09-730-763-16	Sequence 16, Appli
6	283	14.8	54	9 US-09-730-763-15	Sequence 13, Appli
7	276	14.4	54	9 US-09-730-763-18	Sequence 15, Appli
8	273	14.2	52	9 US-09-730-763-27	Sequence 27, Appli
9	273	14.2	52	9 US-09-730-763-28	Sequence 31, Appli
10	271	14.1	52	9 US-09-730-763-31	Sequence 17, Appli
11	271	14.1	54	9 US-09-730-763-17	Sequence 14, Appli
12	270	14.1	54	9 US-09-730-763-14	Sequence 4, Appli
13	267	13.9	338	9 US-09-730-763-34	Sequence 37, Appli
14	267	13.9	338	9 US-09-730-763-37	Sequence 28, Appli
15	262	13.7	52	9 US-09-730-763-28	Sequence 29, Appli
16	260	13.6	52	9 US-09-730-763-29	Sequence 33, Appli
17	254	13.3	54	9 US-09-730-763-33	Sequence 30, Appli
18	254	13.3	52	9 US-09-730-763-33	Sequence 19, Appli
19	247	12.9	52	9 US-09-730-763-30	Sequence 18, Appli

## ALIGNMENTS

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RESULT 1
US-09-988-929A-1
; Sequence 1, Application US/09888929A
; Patent No. US201005982A1
; GENERAL INFORMATION:
; APPLICANT: Brookhaven Science Associates
; APPLICANT: Shanklin, John
; APPLICANT: Cahoon, Edgar B
; TITLE OF INVENTION: Mutant Fatty Acid Desaturase
; FILE REFERENCE: BSA 02-01; CIP of 09/233,856, filed 01/19/99
; CURRENT APPLICATION NUMBER: US/09/988,929A
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 09/233,856
; PRIOR FILING DATE: 1999-01-19
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Ricinus communis
; US-09-988-929A-1

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Best Local Similarity 100.0%; Pred. No. 7.8e-169; Mismatches 0; Indels 0; Gaps 0;
Matches 363; Conservative 0; APPLI 1 ASTLKGSKSKEYENLKKPFMPMPREVHTQVTHSMPPQKIEFSLDNAAEENLVLHLPEVK 60
DB 1 ASTLKGSKSKEYENLKKPFMPMPREVHTQVTHSMPPQKIEFSLDNAAEENLVLHLPEVK 60
QY 61 CWQOPDFLPDASGDFDEQVRLERAKEIPDDYFVVLGDMITEALPTQMLNPLDG 120
DB 61 CWQOPDFLPDASGDFDEQVRLERAKEIPDDYFVVLGDMITEALPTQMLNPLDG 120
QY 121 VRDETAGSPSWAIWTRAWTAENRQDGLNKYLKLYLSGRVDMRQIQTIOYLIGSGMDPR 180
DB 121 VRDETAGSPSWAIWTRAWTAENRQDGLNKYLKLYLSGRVDRQIQTIOYLIGSGMDPR 180
QY 181 TENSPVLFIFTSFQBRATEISHGNNTARQAEFHGDKLQAQICGTTIAADEKRRHETATKIV 240
DB 181 TENSPVLFIFTSFQBRATEISHGNNTARQAEFHGDKLQAQICGTTIAADEKRRHETATKIV 240

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QY 241 EKLEIDPDGTVALADMMRKIKISMPAHMLYDGRDDNLFDHESAVAORLGYTAKDYADI 300  
 Db 241 EKLEIDPDGTVALADMMRKIKISMPAHMLYDGRDDNLFDHESAVAORLGYTAKDYADI 300  
 ; Sequence 2, Application US/09837751  
 ; Patent No. US20020104124A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Green, Allan  
 ; APPLICANT: Singh, Surinder  
 ; APPLICANT: Liu, Qing  
 ; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil  
 ; FILE REFERENCE: 45-00  
 ; CURRENT APPLICATION NUMBER: US/09/837-751  
 ; CURRENT FILING DATE: 2001-04-18  
 ; PRIORITY NUMBER: US 60/198,124  
 ; PRIORITY FILING DATE: 2000-04-18  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 396  
 ; TYPE: PRT  
 ; ORGANISM: Gossypium sp.  
 ; US-09-837-751-2

Query Match 85.4%; Score 1637; DB 10; Length 396;  
 Best Local Similarity 85.1%; Pred. No. 4 Be-143;  
 Matches 308; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

QY 2 STLKGSGKSEVENLKKPMPMPREYVTHSMPQKTEFSLDNWAEINLYHLKPVEKC 61  
 Db 35 STPSPGSEBVGNLKPKPFPKPVQTHSMPPKIEFKSLGWAENINLTHLKPVEKC 94  
 ; Query Match 85.1%; Score 1637; DB 10; Length 396;  
 ; Best Local Similarity 85.1%; Pred. No. 4 Be-143;  
 ; Matches 308; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

QY 62 WQQDFELPDPASDGFDEQVRLERERAKIEDPDDYFVVLVGDMTTEALPTYCQMLNTLDGV 121  
 Db 95 WQQDFELPDPASDGFDEQVRLERERAKIEDPDDYFVVLVGDMTTEALSTYQMLNTLDGT 154  
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 ; Best Local Similarity 85.1%; Pred. No. 4 Be-143;  
 ; Matches 308; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

QY 122 RDETGASPTSWA1WTRWATAENRHGDLINKLYLGSRVDMDQIETKTQYLGSMDPRT 181  
 Db 155 RDETGASPTPWALWTRWATAENRHGDLINKLYLGSRVDMDQIERTKTQYLGSMDPHT 214  
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 ; Best Local Similarity 85.1%; Pred. No. 4 Be-143;  
 ; Matches 308; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

QY 182 ENSPYLGFIYTSQERATEFISHGNTARAKEHDIKLQIOCGTIADEKRHETAYTKE 241  
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 ; Best Local Similarity 100.0%; Pred. No. 7.8e-169;  
 ; Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ; Query Match 100.0%; Score 1916; DB 12; Length 363;  
 ; Best Local Similarity 100.0%; Pred. No. 7.8e-169;  
 ; Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 CWQODPDLPDASDGFDEQVRLERERAKIEDPDDYFVVLVGDMTTEALPTYCQMLNTLDG 120  
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 ; Query Match 100.0%; Score 1916; DB 12; Length 363;  
 ; Best Local Similarity 100.0%; Pred. No. 7.8e-169;  
 ; Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 121 VRDETGASPTSWA1WTRWATAENRHGDLINKLYLGSRVDMDQIETKTQYLGSMDPRT 180  
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 ; Best Local Similarity 100.0%; Pred. No. 7.8e-169;  
 ; Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 TNSPYLGFIYTSQERATEFISHGNTARAKEHDIKLQIOCGTIADEKRHETAYTKE 240  
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 ; Query Match 100.0%; Score 1916; DB 12; Length 363;  
 ; Best Local Similarity 100.0%; Pred. No. 7.8e-169;  
 ; Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 EKLFELPDGTVALADMMRKIKISMPAHMLYDGRDDNLFDHESAVAORLGYTAKDYADI 300  
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 ; Query Match 100.0%; Score 1916; DB 12; Length 363;  
 ; Best Local Similarity 100.0%; Pred. No. 7.8e-169;  
 ; Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ; Query Match 100.0%; Score 1916; DB 12; Length 363;  
 ; Best Local Similarity 100.0%; Pred. No. 7.8e-169;  
 ; Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ; Best Local Similarity 100.0%; Pred. No. 7.8e-169;  
 ; Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4  
 US-09-730-763-12  
 ; Sequence 12, Application US/09730763  
 ; Publication No. US20020192781A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JACKSON, Mary  
 ; APPLICANT: GIQUEL, Brigitte  
 ; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM  
 ; TITLE OF INVENTION: TUBERCULOSIS  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: c/o Finnegan Henderson, Farriarow, Garrett &  
 ; STREET: 1300 I Street, N.W.  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk

RESULT 3  
 US-09-837-751-2

COMPUTER: IBM PC compatible  
 SOFTWARE: PatentsIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/730,763  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/917,299  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MEYERS, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 03495.0156-00  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4400  
 TELEFAX: (202) 408-4400  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 54 amino acids  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-730-763-12

Query Match 15.2%; Score 291; DB 9; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-20;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 US-09-730-763-16

RESULT 6  
 US-09-730-763-13  
 Sequence 13, Application US/09730763  
 Publication No. US20020192781A1

GENERAL INFORMATION:  
 APPLICANT: JACKSON, Mary  
 APPLICANT: GIQUEL, Brigitte  
 TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM  
 TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM  
 NUMBER OF SEQUENCES: 37  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: C/o Finnegan Henderson, Farrabow, Garrett &  
 DUNNER, L.L.P.  
 STREET: 1300 I Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/730,763  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/917,299  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MEYERS, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 03495.0156-00  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4400  
 TELEFAX: (202) 408-4400  
 INFORMATION FOR SEQ ID NO: 13:  
 Sequence 13, Application US/09730763  
 Publication No. US20020192781A1

SEQUENCE CHARACTERISTICS:  
 LENGTH: 54 amino acids  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-730-763-13

Query Match 14.9%; Score 286; DB 9; Length 54;  
 Best Local Similarity 98.1%; Pred. No. 1.1e-19;  
 Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 US-09-730-763-16

RESULT 7  
 US-09-730-763-14  
 Sequence 14, Application US/09730763  
 Publication No. US20020192781A1

GENERAL INFORMATION:  
 APPLICANT: JACKSON, Mary  
 APPLICANT: GIQUEL, Brigitte  
 TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM  
 TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM  
 NUMBER OF SEQUENCES: 37  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: C/o Finnegan Henderson, Farrabow, Garrett &  
 DUNNER, L.L.P.  
 STREET: 1300 I Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/730,763  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/917,299  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MEYERS, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 03495.0156-00  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4400  
 TELEFAX: (202) 408-4400  
 INFORMATION FOR SEQ ID NO: 16:  
 Sequence 16, Application US/09730763  
 Publication No. US20020192781A1

US-09-730-763-15  
 Sequence 15, Application US/09730763  
 Publication No. US20020192781A1  
 GENERAL INFORMATION:  
 APPLICANT: JACKSON, Mary  
 ATTORNEY: GIOQUEL, Brigitte  
 TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM  
 TITLE OF INVENTION: TUBERCULOSIS  
 NUMBER OF SEQUENCES: 37  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: C/o Finnegan Henderson, Farrabow, Garrett & Dunn, L.L.P.  
 STREET: 1300 I Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/730,763  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/917,299  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MEYERS, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 03495.0156-000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4000  
 TELEFAX: (202) 408-4400  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 54 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US-09-730-763-15

RESULT 8  
 us-09-730-763-18  
 Sequence 18, Application US/09730763  
 Publication No. US20020192781A1  
 GENERAL INFORMATION:  
 APPLICANT: JACKSON, Mary  
 ATTORNEY: GIOQUEL, Brigitte  
 TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM  
 TITLE OF INVENTION: TUBERCULOSIS  
 NUMBER OF SEQUENCES: 37  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: C/o Finnegan Henderson, Farrabow, Garrett & Dunn, L.L.P.  
 STREET: 1300 I Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:

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; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-730-763-27

RESULT 11
US-09-730-763-17
; Sequence 17, Application US/09730763
; Publication No. US20020192781A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, Mary
; APPLICANT: GIQUEL, Brigitte
; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O Finnegan Henderson, Farrabow, Garrett &
; STREET: Dunner, L.L.P.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Re-Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,763
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/917,299
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0156-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-730-763-17

Query Match 14.1%; Score 271; DB 9; Length 52;
Best Local Similarity 98.1%; Pred. No. 2.5e-18;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-730-763-31

RESULT 10
US-09-730-763-31
; Sequence 31, Application US/09730763
; Publication No. US20020192781A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, Mary
; APPLICANT: GIQUEL, Brigitte
; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/o Finnegan Henderson, Farrabow, Garrett &
; STREET: Dunner, L.L.P.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Re-Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,763
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/917,299
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0156-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-730-763-17

Query Match 14.1%; Score 271; DB 9; Length 54;
Best Local Similarity 90.7%; Pred. No. 2.6e-18;
Matches 49; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-730-763-31

RESULT 12
US-09-730-763-14
; Sequence 14, Application US/09730763
; Publication No. US20020192781A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, Mary
; APPLICANT: GIQUEL, Brigitte
; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/o Finnegan Henderson, Farrabow, Garrett &
; STREET: Dunner, L.L.P.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Re-Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,763
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/917,299
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0156-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-730-763-31

Query Match 14.1%; Score 271; DB 9; Length 52;
Best Local Similarity 98.1%; Pred. No. 2.5e-18;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-730-763-31

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COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/730,763  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/917,299  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MEYERS, Kenneth J.  
 REGISTRATION NUMBER: 03495.0156-00  
 REFERENCE/DOCKET NUMBER: 03495.0156-00  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4000  
 TELEFAX: (202) 408-4400  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 54 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-730-763-14

Query Match 14.1%; Score 270; DB 9; Length 54;  
 Best Local Similarity 92.6%; Pred. No. 3.e-18;  
 Matches 50; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 98 LVGDMITEALPYQTMLNTLDGVDRTEGASPTSWAIWTRAWTAEENRHGDLLN 151  
 Db 1 LVGDMITEALPYQTMLNTLDGVDRTEGASPTSWAIWTRAWTAEENRHGDLLH 54

RESULT 13  
 US-09-730-763-4  
 Sequence 4, Application US/09710763  
 Publication No. US/0020192781A1  
 GENERAL INFORMATION:  
 APPLICANT: JACKSON, Mary  
 APPLICANT: GIQUEL, Brigitte  
 TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM  
 NUMBER OF SEQUENCES: 37  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: C/o Finnegan Henderson, Farrabow, Garrett &  
 ADDRESSEE: Dunner, L.L.P.  
 STREET: 1300 I Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/730,763  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/917,299  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MEYERS, Kenneth J.  
 REFERENCE/DOCKET NUMBER: 03495.0156-00  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 338 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-730-763-4

Query Match 13.9%; Score 267; DB 9; Length 338:  
 Best Local Similarity 25.6%; Pred. No. 9.3e-17;  
 Matches 84; Conservative 54; Mismatches 128; Indels 62; Gaps 11;

Qy 19 MPREHVQVTHSMPPKIEFKSLDNAAEENILVHKPVEKWCQPODFLPPASDG--- 75  
 Db 1 MSAKLTQIQLHELP-----VVERLYNRLHLSMH----KPNHDYI--PWSDGKNY 46  
 Qy 76 -----FDEQVRELREBAKEPDYFVVLGDMITEBALPYQ---TMLNTLDGVDRDET 125  
 Db 47 YALGGQDNDPDSKLSDVAQ-----VAMQNVLNTDLSYHRETAMNGMDG---- 94  
 Qy 126 GASPTSWAIWTRAWTAEENRHGDLLNLYLSGRVDMRQIETQVJGSGNDPRTENSP 185  
 Db 95 -----ANGQWVWRWTABENRHTALDYLVVRPSVDELEKLRLEVNRGSPGQNHQG 149  
 Qy 186 YL-----GFIYTSQERATEFISHGNTARQAKEHGDIKLAIQCGTTAADERKRHETAY'K 238  
 Qy 150 HYFAESELTSVYVSQELATFISHRT---SKACNDPVAQDOLMAKTSADENLHMITYRD 206  
 Db 207 VSEAAFDLVPN-----QAMSLSHLILSHFQMPGQFQYEFRRKAVVIAVGGVYDPRHL 259

RESULT 14  
 US-09-730-763-37  
 Sequence 37, Application US/09730763  
 Publication No. US/0020192781A1  
 GENERAL INFORMATION:  
 APPLICANT: JACKSON, Mary  
 APPLICANT: GIQUEL, Brigitte  
 TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM  
 NUMBER OF SEQUENCES: 37  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: C/o Finnegan Henderson, Farrabow, Garrett &  
 ADDRESSEE: Dunner, L.L.P.  
 STREET: 1300 I Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/730,763  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/917,299  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MEYERS, Kenneth J.  
 REFERENCE/DOCKET NUMBER: 25.146  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4000

; TELEPHONE: (202) 408-4000  
 ; TELEFAX: (202) 408-4400  
 ; INFORMATION FOR SEQ ID NO: 37:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 37 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-730-763-37

; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 408-4000  
 ; TELEFAX: (202) 408-4400  
 ; INFORMATION FOR SEQ ID NO: 28:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 52 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-09-730-763-28

Query Match 13.9%; Score 267; DB 9; Length 338;  
 Best Local Similarity 25.6%; Pred. No. 9.3e-17;  
 Matches 84; Conservative 54; Mismatches 128; Indels 62; Gaps 11;

Qy 19 MPPREHIVQVTHSMPPQEIEFKSLDNWAENILVHLKPVERCWQPODFLPDPASDG-- 75  
 Db 1 MSAKLTDLQILHELEP----VVEKYLNRLHSMH---KPWNPHDI--PWSDGKNY 46

Qy 76 -----FDEQYRELRLERAKAEIFPDDYFVVLYGDMITEEALPYYQ--TMILNLTDGYRDET 125  
 Db 47 YALGGQDWDPPDKSLSDVQ-----VAVMONLYLTDNLPAHYRETAMNGMDG --- 94

Qy 126 GASPTSWAIWTRAWTAENRHGDLNNKYLISGRVDMRQIETKIQYLIGSGMDPRTENSP 185  
 Db 95 -----ANGQWNRWTAENRHGTLALRYYVTRSDVPVLEKLRLLEVNRGSPQNHOG 149

Qy 186 YL-----GFIYTSFQFRATFISHGNTAERQAKEHGDIKLQAOICGTTIAADEKRHETAYK 238  
 Db 150 HYFAESLTDSVLYVSQFELATRISHRNT--GKACNDPVAOLMAKSADENLHMFYRD 206

Qy 239 IVEKLFELDPDGTVLAPADMRRKIKSMPAHLMYGDRDDNLFDHESAVAQRLGVYTAKDYA 298  
 Db 207 VSEAADFIVPN-----QAMKSLHLIISHPOMPGEQYFPEFRKAVVAVGGVYDRIHL 259

Qy 299 D-TLEFLVYRKVDKLTLGTLGSAEQAQD 325  
 Db 260 DEVVMPVLKKNCTIFEREDFTGEAKLKD 287

RESULT 15  
 US-09-730-763-28  
 ; Sequence 28, Application US/09730763  
 ; Publication No. US20020192781A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JACKSON, Mary  
 ; APPLICANT: GIQUEL, Brigitte  
 ; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM  
 ; TITLE OF INVENTION: TUBERCULOSIS  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: c/o Finnegan Henderson, Farrabow, Garrett &  
 ; STREET: Dunner, L.L.P.  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/730,763  
 ; FILING DATE:  
 ; CLASIFICATION:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/917,299  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: MEYERS, Kenneth J.  
 ; REGISTRATION NUMBER: 25,146  
 ; REFERENCE/DOCKET NUMBER: 03495.0156-00

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Db 34 ASTLKGSKSEVENLKKPFMPPREVHQVTHSMPPQKIEFKSLDNWAEENILVHLKPEVK 93  
 Qy 61 CNOPODFLPDPASDGFDEVREAKEIPDDYFVVYLVGDMITEEALPTYCOTMLNTLDG 1.20  
 Db 94 CNOQDFLDPASDGFDEVREAKEIPDDYFVVYLVGDMITEEALPTYCOTMLNTLDG 1.53  
 Qy 121 VDETGTASPTSWAIWTRWTAEEENRGDLNKKYLIGSGMDPR 1.80  
 Db 154 VDETGTASPTSWAIWTRWTAEEENRGDLNKKYLIGSGMDPR 2.13  
 Qy 181 TENSPLYGFIIYTSQERATFISHGNTARQAKEHGDIKLAQICGTTIADEKRHETAYTKIV 2.40  
 Db 214 TENSPLYGFIIYTSQERATFISHGNTARQAKEHGDIKLAQICGTTIADEKRHETAYTKIV 2.73  
 Qy 241 EKLEFEIDDDGTYLAFADMNRKKTSMPAHMLYDGRDDNLFDHSAVQLGVYTAKDADI 3.00  
 Db 274 EKLEFEIDDDGTYLAFADMNRKKTSMPAHMLYDGRDDNLFDHSAVQLGVYTAKDADI 3.33  
 Qy 301 LEFLVGRKVKDUTGLSAGQKADYVCRLLPPIRRLERAGRAKEAPTMPFSWIFDRO 3.60  
 Db 334 LEFLVGRKVKDUTGLSAGQKADYVCRLLPPIRRLERAGRAKEAPTMPFSWIFDRO 3.93  
 Qy 361 VKL 363  
 Db 394 VKL 396

Db 34 ASTLKGSKSEVENLKKPFMPPREVHQVTHSMPPQKIEFKSLDNWAEENILVHLKPEVK 93  
 Qy 61 CNOPODFLPDPASDGFDEVREAKEIPDDYFVVYLVGDMITEEALPTYCOTMLNTLDG 1.20  
 Db 94 CNOQDFLDPASDGFDEVREAKEIPDDYFVVYLVGDMITEEALPTYCOTMLNTLDG 1.53  
 Qy 121 VDETGTASPTSWAIWTRWTAEEENRGDLNKKYLIGSGMDPR 1.80  
 Db 154 VDETGTASPTSWAIWTRWTAEEENRGDLNKKYLIGSGMDPR 2.13  
 Qy 181 TENSPLYGFIIYTSQERATFISHGNTARQAKEHGDIKLAQICGTTIADEKRHETAYTKIV 2.40  
 Db 214 TENSPLYGFIIYTSQERATFISHGNTARQAKEHGDIKLAQICGTTIADEKRHETAYTKIV 2.73  
 Qy 241 EKLEFEIDDDGTYLAFADMNRKKTSMPAHMLYDGRDDNLFDHSAVQLGVYTAKDADI 3.00  
 Db 274 EKLEFEIDDDGTYLAFADMNRKKTSMPAHMLYDGRDDNLFDHSAVQLGVYTAKDADI 3.33  
 Qy 301 LEFLVGRKVKDUTGLSAGQKADYVCRLLPPIRRLERAGRAKEAPTMPFSWIFDRO 3.60  
 Db 334 LEFLVGRKVKDUTGLSAGQKADYVCRLLPPIRRLERAGRAKEAPTMPFSWIFDRO 3.93  
 Qy 361 VKL 363  
 Db 394 VKL 396

RESULT 3  
 US-08-329-560-3  
 ; Sequence 3, Application US/08329560  
 ; Patent No. 5654402  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CAHOON, Edgar B.  
 ; ADDRESS: 700 Capital Square, 400 Locust Street  
 ; CITY: Des Moines  
 ; STATE: Iowa  
 ; ZIP: 50309  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patenter Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/329.560  
 ; FILING DATE: 26-OCT-1994  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Yates, Michael E.  
 ; REGISTRATION NUMBER: 36, 063  
 ; REFERENCE/DOCKET NUMBER: 0284US  
 ; TELEPHONE: (515) 248-4800  
 ; TELEFAX: (515) 248-4844  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 396 amino acids  
 ; TYPE: amino acid  
 ; STRANDDNESS:  
 ; TOPOLOGY: linear  
 ; Query Match 100.0% Score 1916; DB 1; Length 396;  
 ; Best Local Similarity 100.0% Pred. No. 2, z=180;  
 ; Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 ; Qy 1 ASTLKGSKSEVENLKKPFMPPREVHQVTHSMPPQKIEFKSLDNWAEENILVHLKPEVK 60

REGISTRATION NUMBER: 31,845  
 REGISTRATION NUMBER: 34,719  
 NAME: Carl J. Schwedler  
 REFERENCE/DOCKET NUMBER: 36,924  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (916) 753-6313  
 TELEFAX: (916) 753-1510  
 TELEX: 350370 CGNE  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 396 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-471-791-16

Query Match 100.0%; Score 1916; DB 1; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-180;  
 Matches 363; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 ASTLKGSSKEVENLKKPMPREHYQVTHSMPPQKIEFKSLDNWAEEENLVLHKPVEK  
 Db 34 ASTLKGSSKEVENLKKPMPREHYQVTHSMPPQKIEFKSLDNWAEEENLVLHKPVEK 93

Qy 61 CWQPODFLPDPASGDFDEVRELRAKEIPDDYFVVLGDMITEALPQTOMLNTLDG 120  
 Db 94 CWQPODFLPDPASGDFDEVRELRAKEIPDDYFVVLGDMITEALPQTOMLNTLDG 153

Qy 121 VRDETAGSPTSWAIVTRAWTAEENRHGDLLANKYLGSRYDMRQEKTQIQLIGSGMDPR 180  
 Db 154 VRDETAGSPTSWAIVTRAWTAEENRHGDLLANKYLGSRYDMRQEKTQIQLIGSGMDPR 213

Qy 181 TNSPYLGFITYTSFQERATFISHGNTARQAEKGDIKLAICGTTIAADEKRHETAYTKIV 240  
 Db 214 TNSPYLGFITYTSFQERATFISHGNTARQAEKGDIKLAICGTTIAADEKRHETAYTKIV 273

Qy 241 EKLFIEDPDGTWLAFADEMMRKKISMPAHLYMDGRDNLFHESAYAQRQLGYYTAKYADI 300  
 Db 274 EKLFIEDPDGTWLAFADEMMRKKISMPAHLYMDGRDNLFHESAYAQRQLGYYTAKYADI 333

Qy 301 LEFLVGRWKVDKLGLSAGOGKAQDYVCRLPPIRRIEERAGRAKEAPTMPSWIFDQ 360  
 Db 334 LEFLVGRWKVDKLGLSAGOGKAQDYVCRLPPIRRIEERAGRAKEAPTMPSWIFDQ 393

RESULT 4  
 US-08-926-522-4

Sequence 4, Application US/08926522  
 Patent No. 6426447  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Calgene, Inc.  
 STREET: 1920 Fifth Street  
 CITY: Davis  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 95616  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Macintosh 7.1  
 SOFTWARE: Microsoft Word 5.1(a)  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/926,522  
 FILING DATE:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/458,173  
 FILING DATE: 2-June-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Elizabeth Lassen  
 REGISTRATION NUMBER: 31,845  
 NAME: Donna E. Scherer  
 REGISTRATION NUMBER: 34,719  
 NAME: Carl J. Schwedler  
 REGISTRATION NUMBER: 36,924  
 REFERENCE/DOCKET NUMBER: CGNE DES  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (916) 753-6313  
 TELEFAX: (916) 753-1510  
 INQUIRIES FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 396 amino acids  
 TYPE: amino acid  
 MOLECULE TYPE: protein

US-08-926-522-4

Query Match 100.0%; Score 1916; DB 1; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-180;  
 Matches 363; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 ASTLKGSSKEVENLKKPMPREHYQVTHSMPPQKIEFKSLDNWAEEENLVLHKPVEK 60  
 Db 34 ASTLKGSSKEVENLKKPMPREHYQVTHSMPPQKIEFKSLDNWAEEENLVLHKPVEK 93

Qy 61 CWQPODFLPDPASGDFDEVRELRAKEIPDDYFVVLGDMITEALPQTOMLNTLDG 120  
 Db 94 CWQPODFLPDPASGDFDEVRELRAKEIPDDYFVVLGDMITEALPQTOMLNTLDG 153

Qy 121 VRDETAGSPTSWAIVTRAWTAEENRHGDLLNKYLGSRVDMRQEKTQIQLIGSGMDPR 180  
 Db 154 VRDETAGSPTSWAIVTRAWTAEENRHGDLLNKYLGSRVDMRQEKTQIQLIGSGMDPR 213

Qy 181 TNSPYLGFITYTSFQERATFISHGNTARQAEKGDIKLAICGTTIAADEKRHETAYTKIV 240  
 Db 214 TNSPYLGFITYTSFQERATFISHGNTARQAEKGDIKLAICGTTIAADEKRHETAYTKIV 273

Qy 241 EKLFIEDPDGTWLAFADEMMRKKISMPAHLYMDGRDNLFHESAYAQRQLGYYTAKYADI 300  
 Db 274 EKLFIEDPDGTWLAFADEMMRKKISMPAHLYMDGRDNLFHESAYAQRQLGYYTAKYADI 333

Qy 301 LEFLVGRWKVDKLGLSAGOGKAQDYVCRLPPIRRIEERAGRAKEAPTMPSWIFDQ 360  
 Db 334 LEFLVGRWKVDKLGLSAGOGKAQDYVCRLPPIRRIEERAGRAKEAPTMPSWIFDQ 393

RESULT 5  
 PCT-US91-01746-16  
 Sequence 16, Application PC/TUS9101746  
 GENERAL INFORMATION:  
 APPLICANT: Thompson, Gregory A  
 TITLE OF INVENTION: Plant Desaturases-Compositions and Uses  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Calgene, Inc.  
 STREET: 1920 Fifth Street  
 CITY: Davis  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 95616  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Macintosh 7.1  
 SOFTWARE: Microsoft Word 5.1(a)  
 CURRENT APPLICATION DATA:

COMPUTER READABLE FORM:  
 COMPUTER: Apple Macintosh, 3.50 inch, 1.0 MB storage  
 OPERATING SYSTEM: Macintosh 6.0.7  
 SOFTWARE: MicrosoftWord 4.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US91/01746  
 FILING DATE: 19910314  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/615,784  
 FILING DATE: 14 NOV-1990  
 APPLICATION NUMBER: 07/567,373  
 FILING DATE: 13-AUG-1990  
 APPLICATION NUMBER: 07/494,106  
 FILING DATE: 16 MAR-1990  
 NAME: Lassen, Elizabeth  
 REGISTRATION NUMBER: 31,845  
 NAME: Donna E. Scherer  
 REGISTRATION NUMBER: 34,719  
 REFERENCE/DOCKET NUMBER: CGNE 69-3 WO  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (916) 753-6313  
 TELEFAX: (916) 753-1510  
 TELEX: 250370 CGNE  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 396 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US91-01746-16

Query Match 100.0%; Score 1916; DB 5; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-180;  
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKKEVENLKKPMPMPREYHQVTHSMPPQKIEFKSLDNWAENILVHLKPEK 60

Db 34 ASTLKSGSKKEVENLKKPMPMPREYHQVTHSMPPQKIEFKSLDNWAENILVHLKPEK 93

Qy 61 CWQPODFLPASDGFDEVRLERAKEPDDYFVVLGDMITEALPTYQTMNLTLG 120

Db 94 CWQPODFLPASDGFDEVRLERAKEPDDYFVVLGDMITEALPTYQTMNLTLG 153

Qy 121 VRDETGASPTSWATWTRANTAEENRHGDLLNKYLISGRVDMRQEKTQYLIGSM DPR 180

Db 154 VRDETGASPTSWATWTRANTAEENRHGDLLNKYLISGRVDMRQEKTQYLIGSM DPR 213

Qy 181 TENSPLYLGFTTSFOERATFISHNTARAKEHGDIKLAQICGTTIAADEKRHETAYTKIV 240

Db 214 TENSPLYLGFTTSFOERATFISHNTARAKEHGDIKLAQICGTTIAADEKRHETAYTKIV 273

Qy 241 EKLEFIDPDGTVALADMMRKKISMPAHLMYGRDDNLDFHSAVAQRQGRAKEAFTMPFSWIFDQ 300

Db 274 EKLEFIDPDGTVALADMMRKKISMPAHLMYGRDDNLDFHSAVAQRQGRAKEAFTMPFSWIFDQ 333

Qy 301 LEFLVGRWKVDKLTLGSAEQQKAQDYVCRLPPIRRLEREAQGRAKEAFTMPFSWIFDQ 360

Db 334 LEFLVGRWKVDKLTLGSAEQQKAQDYVCRLPPIRRLEREAQGRAKEAFTMPFSWIFDQ 393

Qy 361 VKL 363

Db 394 VKL 396

APPLICANT: Yadav, Narendra S.  
 APPLICANT: Perez, Grau, Luis  
 TITLE OF INVENTION: Nucleotide Sequence of  
 TITLE OF INVENTION: Soybean Stearyl-ACP  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: E. I. du Pont de Nemours  
 and Company  
 STREET: 1007 Market Street  
 CITY: Wilmington  
 STATE: Delaware  
 COUNTRY: U.S.A.  
 ZIP: 19898  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
 COMPUTER: Macintosh System, 6.0  
 OPERATING SYSTEM: Macintosh System, 6.0  
 SOFTWARE: Microsoft Word, 4.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/995,657  
 FILING DATE: 19921211  
 FILING DATE: C) CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: GEIGER, KATHLEEN W.  
 REGISTRATION NUMBER: 35,880  
 REFERENCE/DOCKET NUMBER: BB\_1022-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 302-892-8112  
 TELEFAX: 302-892-7949  
 TELEX: 835420  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 391 amino acids  
 TYPE: AMINO ACID  
 STRANDEDNESS: unknown  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-07-995-657-6

Query Match 91.5%; Score 1753; DB 1; Length 391;  
 Best Local Similarity 89.8%; Pred. No. 2.4e-164;  
 Matches 326; Conservative 24; Mismatches 13; Indels 0; Gaps 0;  
 Qy 1 ASTLKSGSKKEVENLKKPMPMPREYHQVTHSMPPQKIEFKSLDNWAENILVHLKPEK 60  
 Db 29 ASTLKSGSKKEVENLKKPMPMPREYHQVTHSMPPQKIEFKSLDNWAENILVHLKPEK 88  
 Qy 61 CWQPODFLPASDGFDEVRLERAKEPDDYFVVLGDMITEALPTYQTMNLTLG 120  
 Db 89 CWQPODFLPASDGFDEVRLERAKEPDDYFVVLGDMITEALPTYQTMNLTLG 148  
 Qy 121 VRDETGASPTSWATWTRANTAEENRHGDLLNKYLISGRVDMRQEKTQYLIGSM DPR 180  
 Db 149 VRDETGASPTSWATWTRANTAEENRHGDLLNKYLISGRVDMRQEKTQYLIGSM DPR 208  
 Qy 181 TENSPLYLGFTTSFOERATFISHNTARAKEHGDIKLAQICGTTIAADEKRHETAYTKIV 240  
 Db 269 EKLEFIDPDGTVALADMMRKKISMPAHLMYGRDDNLDFHSAVAQRQGRAKEAFTMPFSWIFDQ 360  
 Qy 209 TENSPLYLGFTTSFOERATFISHNTARAKEHGDIKLAQICGTTIAADEKRHETAYTKIV 268  
 Qy 241 EKLEFIDPDGTVALADMMRKKISMPAHLMYGRDDNLDFHSAVAQRQGRAKEAFTMPFSWIFDQ 300  
 Db 269 EKLEFIDPDGTVALADMMRKKISMPAHLMYGRDDNLDFHSAVAQRQGRAKEAFTMPFSWIFDQ 333  
 Qy 301 LEFLVGRWKVDKLTLGSAEQQKAQDYVCRLPPIRRLEREAQGRAKEAFTMPFSWIFDQ 360  
 Qy 334 LEFLVGRWKVDKLTLGSAEQQKAQDYVCRLPPIRRLEREAQGRAKEAFTMPFSWIFDQ 393  
 Qy 361 VKL 363  
 Db 394 VKL 396

RESULT 6  
 US-07-995-657-6  
 Sequence 6, Application US/07995657  
 Patent No. 5443974  
 GENERAL INFORMATION:  
 APPLICANT: Hitz, William D.

RESULT 7

US-08-474-587-6 Sequence 6, Application US/08474587  
Patent No. 5760206

GENERAL INFORMATION:

APPLICANT: Hitz, William D.  
APPLICANT: Yadav, Narendra S.  
APPLICANT: Perez-Grau, Luis

TITLE OF INVENTION: Nucleotide Sequence of

Patent No. 5760206

TITLE OF INVENTION: Soybean Stearyl-ACP Desaturase cDNA

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS: E. I. du Pont de Nemours

ADDRESSEE: and Company

STREET: 1007 Market Street

CITY: Wilmington

STATE: Delaware

ZIP: 19898

COMPUTER READABLE FORM:

COMPUTER: Macintosh

OPERATING SYSTEM: Macintosh System, 6.0

SOFTWARE: Microsoft Word, 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,587

FILED DATE: 1998-01-20

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 5760206

FILED DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Siegell, Barbara C.

REGISTRATION NUMBER: 30,684

REFERENCE/DOCKET NUMBER: BB\_1022-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 302-992-4931

TELEFAX: 302-773-0164

TELEX: 835420

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 391 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-474-587-6

Query Match 91.5%; Score 1753; DB 1; Length 391;  
Best Local Similarity 89.8%; Pred. No. 2, 4e-164;  
Matches 326; Conservative 24; Mismatches 13; Indels 0; Gaps 0;

Qy 1 CWOQDPLPASDGFDEQVRRLERAKEIPDDYFVVLVGDMITEALPTQMLMLDG 120  
Db 89 CWOQDPLPDPSSDGFPEQVKLERAKEIPDDYFVVLVGDMITEALPTQMLMLDG 148

Qy 29 ASTLRSSEKVEENIKKPFTPPREVHQVTHSMAPPQKIEFKSLEDWADQNLTTHLPKEK 88

Qy 61 CWOQDPLPASDGFDEQVRRLERAKEIPDDYFVVLVGDMITEALPTQMLMLDG 120  
Db 89 ASTLRSSEKVEENIKKPFTPPREVHQVTHSMAPPQKIEFKSLEDWADQNLTTHLPKEK 88

Qy 121 VRDETAGSPTSAIWPRTAEENRHDLNLKYLSGRVDMRQIEKTQVQLGSGMDPR 180

Db 149 VRDETAGSPTSAIWPRTAEENRHDLNLKYLSGRVDMKQIEKTQVQLGSGMDPR 208

Qy 181 TNSPYLGFITTSQERATFISHGNTARQAEHGDKLAQICGTTIADEKRHETATKIV 240

Db 209 TNSPYLGFITTSQERATFISHGNTARLAKBHDIKLQICGTMASDEKRHETATKIV 268

Qy 241 EKLFELIDDPGTVLAFADMMRKKISMPPAHLMYDGRDNLFHESAVAOQLGYTTAKDYADI 300  
Db 269 EKLFELIDDPGTVMAFDAMMRKKAIPAHLMYDGRDNLFHESAVAOQLGYTTAKDYADI 328

Qy 301 LEFLVGRMKVDKLTLGELSAGQKAQDYVCRLLPRTRIILERAGRAKEAPTMPSWFDQ 360  
Db 329 LEFLVGRMKVQEQLTGSSEGRKAQEVYVGLPPTRIILERAGRQESSTLKFSWHDRE 388

Qy 361 VKL 363

Db 389 VLL 391

RESULT 8

US-08-471-791-13

Sequence 13, Application US/08471791  
Patent No. 572595

GENERAL INFORMATION:

APPLICANT: Thompson, Gregory A.  
APPLICANT: Knauf, Vic C

TITLE OF INVENTION: Plant Desaturases-Compositions

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Calgene, Inc.

STREET: 1920 Fifth Street

CITY: Davis

STATE: California

ZIP: 95616

COMPUTER READABLE FORM:

COMPUTER: Apple Macintosh

MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage

OPERATING SYSTEM: Macintosh 7.1

SOFTWARE: Microsoft Word 5.1 (a)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,791

FILING DATE: 6-JUNE-95

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/762,762

FILING DATE: 16-SEPT-1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/471,791

FILING DATE: 14-NOV-1990

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/567,373

FILING DATE: 13-AUG-1990

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/494,106

FILING DATE: 16-MAR-1990

ATTORNEY/AGENT INFORMATION:

NAME: Lassen, Elizabeth

REGISTRATION NUMBER: 31,845

NAME: Donna E. Scherer

REGISTRATION NUMBER: 34,719

NAME: Carl J. Schwedler

REGISTRATION NUMBER: 36,924

REFERENCE/DOCKET NUMBER: CGNE 69-5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (916) 753-6313

TELEFAX: (916) 753-1510

TELEX: 350370 CGNE

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 396 amino acids

TYPE: amino acid

TOPOLOGY: linear



```

; SOFTWARE : Microsoft Word 5.1 (a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,791
; FILING DATE: 6-JUNE-95
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01746
; FILING DATE: 14-MAR-1991
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/762,762
; FILING DATE: 16-SEPT-1991
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01746
; FILING DATE: 14-MAR-1991
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/615,784
; FILING DATE: 14-NOV-1990
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/567,373
; FILING DATE: 13-AUG-1990
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/494,106
; FILING DATE: 16-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lassen, Elizabeth
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE 69-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; TELEX: 350570 CGNE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-471-791-20

Query Match 88.6%; Score 1698; DB 1; Length 398;
Best Local Similarity 88.2%; Pred. No. 6.3e-159;
Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

Qy 8 SKEVENLNKPMPREPVHQVTHSMPPKIEIFKSLDNWAEENYLVHLKPVERKCMWQFD 67
Db 43 LPDPASDGFQDQEYRERAKEIPLDYFVVLGDMITEEALPYQTMNLNTLGVRD 67
Qy 68 LPDPASDGFQDQEYRERAKEIPLDYFVVLGDMITEEALPYQTMNLNTLGVRD 67
Db 103 LPDPASDGFQDQEYRERAKEIPLDYFVVLGDMITEEALPYQTMNLNTLGVRD 67
Qy 128 SPITSWAIWTRWAAENRHDLNKLYLSPGRVDMRQIETKIQYLIGSGMDPRTE 187
Db 163 SPITSWAIWTRWAAENRHDLNKLYLSPGRVDMRQIETKIQYLIGSGMDPRTE 187
Qy 188 GFYTSFQFRATISHGNARQAEKGDKLIAOICGTTIADEKRHETAYTKIVEKLF 247
Db 223 GFYTSFQFRATISHGNARQAEKGDKLIAOICGTTIADEKRHETAYTKIVEKLF 247
Qy 248 PDGTVLAFADMMRKKISMPAHLMYGDGRDNLDPHESAYAQLRGVYTAKDYADLFL 307
Db 283 PDGTVMAFFADMMRKKISMPAHLMYGDGRSLFDNFNSAYAQLRGVYTAKDYADLFL 342
Qy 308 WKVDKLIGSAGQKAQDWCRLPRTIRLEPAQGRKAEAPDMPFWSMFDQVKL 363
Db 343 WKTSILTGSEGKNAQETLGLTPRIRLDERAQRARKKGPKVPPSWHIDREVQL 398

RESULT 12
US-08-922-522-6

```

Sequence 6, Application US/08926522  
 Patent No. 6426547  
 GENERAL INFORMATION:  
 APPLICANT: Vic C. Knauf  
 APPLICANT: Gregory A. Thompson  
 TITLE OF INVENTION: PLANT SEED OILS  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Calgene, Inc.  
 STREET: 1920 Fifth Street  
 CITY: Davis  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 95616  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Macintosh 7.1  
 SOFTWARE: Microsoft Word 5.1(a)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/926,522  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/458,173  
 FILING DATE: 2-June-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Elizabeth Lassen  
 REGISTRATION NUMBER: 31,845  
 NAME: Donna E. Scherer  
 REGISTRATION NUMBER: 34,719  
 NAME: Carl J. Schwedler  
 REGISTRATION NUMBER: 36,924  
 REFERENCE/DOCKET NUMBER: CGNE DES  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (916) 753-6313  
 TELEFAX: (916) 753-1510  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 398 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-926-522-6

Query Match 88.6%; Score 1698; DB 4; Length 398;  
 Best Local Similarity 88.2%; Pred. No. 6, 3e-159;  
 Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

Qy 8 SKEVENLKPKFMPREHVQVTHSMPPQKIEFKSLDNWAENILVHLKPVEKWCWQDF 67  
 Db 43 SKEVESLKPKFPPKEVHQVHSMPQKIEFKSLDNWAENILVHLKPVEKWCWQDF 102

Qy 68 LPDPASDFGDFQRELREKAPKLPDDYFVVLGDMITEALPTYQTMINTLGVRDETGA 127  
 Db 103 LPDPASDFGDFQRELREKAPKLPDDYFVVLGDMITEALPTYQTMINTLGVRDETGA 162

Qy 128 SPTSWA1WTRWAAENRHGDLINKYLSSGVDMDPTEKTYLIGSGMDPRTENSPYL 187  
 Db 163 SPTSWA1WTRWAAENRHGDLINKYLSSGVDMDPTEKTYLIGSGMDPRTENSPYL 222

Qy 188 GFIYTSQERATFISHGNTARQAKEHGDIAKQICGTTAADERKRHETAYTKIVEKLFIED 247  
 Db 223 GFIYTSQERATFISHGNTARQAKEHGDIAKQICGTTAADERKRHETAYTKIVEKLFIED 282

Qy 248 PGDTVLAFADMRRKKISMPAHLYMDGRDDNLFDHFSAYAORLGVTAKDYADILEFLVGR 307  
 Db 283 PGDTVMFAFDMRRKKISMPAHLYMDGRDLSFNSAQRQLGVTAKDYADILEFLVGR 342

Qy 308 WKVDKTLGLSAECQAKDYVCPLPPIRRLERQGRAKEATMPESWIFDQVKL 363  
 Db 343 WKTESLGLSGEGNKAQEYLCLGLTPRIRRLDRAQAKKGKVPSWIDOREVQL 398

RESULT 13  
 PCT-US91-01746-20  
 Sequence 20, Application PC/TUS9101746  
 GENERAL INFORMATION:  
 APPLICANT: Thompson, Gregory A  
 APPLICANT: Knauf, Vic C  
 TITLE OF INVENTION: Plant Desaturases-Compositions and Uses  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Calgene, Inc.  
 STREET: 1920 Fifth Street  
 CITY: Davis  
 STATE: California  
 COUNTRY: USA  
 ZIP: 95616  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Macintosh 6.0.7  
 SOFTWARE: MicrosoftWord 4.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US91/01746  
 FILING DATE: 19910314  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/615,784  
 FILING DATE: 14-NOV-1990  
 APPLICATION NUMBER: 07/567,373  
 FILING DATE: 13-AUG-1990  
 APPLICATION NUMBER: 07/494,106  
 FILING DATE: 16-MAR-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lassen, Elizabeth  
 REGISTRATION NUMBER: 31,845  
 NAME: Donna E. Scherer  
 REGISTRATION NUMBER: 34,719  
 REFERENCE/DOCKET NUMBER: CGNE 69-3 WO  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (916) 753-6313  
 TELEFAX: (916) 753-1510  
 TELEX: 356370 CGNE  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 398 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US91-01746-20

Query Match 88.6%; Score 1698; DB 5; Length 398;  
 Best Local Similarity 88.2%; Pred. No. 6, 3e-159; Mismatches 15; Indels 0; Gaps 0;

Qy 8 SKEVENLKPKFMPREHVQVTHSMPPQKIEFKSLDNWAENILVHLKPVEKWCWQDF 67  
 Db 314; Conservative Matches 314; Mismatches 27; Indels 0; Gaps 0;

Qy 8 SKEVENLKPKFMPREHVQVTHSMPPQKIEFKSLDNWAENILVHLKPVEKWCWQDF 67  
 Db 43 SKEVESLKPKFPPKEVHQVHSMPQKIEFKSLDNWAENILVHLKPVEKWCWQDF 102

Qy 68 GFIYTSQERATFISHGNTARQAKEHGDIAKQICGTTAADERKRHETAYTKIVEKLFIED 127  
 Db 103 GFIYTSQERATFISHGNTARQAKEHGDIAKQICGTTAADERKRHETAYTKIVEKLFIED 162

Qy 128 SPTSWA1WTRWAAENRHGDLINKYLSSGVDMDPTEKTYLIGSGMDPRTENSPYL 187  
 Db 163 SPTSWA1WTRWAAENRHGDLINKYLSSGVDMDPTEKTYLIGSGMDPRTENSPYL 222

Qy 188 GFIYTSQERATFISHGNTARQAKEHGDIAKQICGTTAADERKRHETAYTKIVEKLFIED 247  
 Db 223 GFIYTSQERATFISHGNTARQAKEHGDIAKQICGTTAADERKRHETAYTKIVEKLFIED 282

Qy 248 PGDTVLAFADMRRKKISMPAHLYMDGRDDNLFDHFSAYAORLGVTAKDYADILEFLVGR 307  
 Db 283 PGDTVMFAFDMRRKKISMPAHLYMDGRDLSFNSAQRQLGVTAKDYADILEFLVGR 342

Qy 308 WKVDKTLGLSAECQAKDYVCPLPPIRRLERQGRAKEATMPESWIFDQVKL 363  
 Db 343 WKTESLGLSGEGNKAQEYLCLGLTPRIRRLDRAQAKKGKVPSWIDOREVQL 398

RESULT 13  
 PCT-US91-01746-20  
 Sequence 20, Application PC/TUS9101746  
 GENERAL INFORMATION:  
 APPLICANT: Thompson, Gregory A  
 APPLICANT: Knauf, Vic C  
 TITLE OF INVENTION: Plant Desaturases-Compositions and Uses  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Calgene, Inc.  
 STREET: 1920 Fifth Street  
 CITY: Davis  
 STATE: California  
 COUNTRY: USA  
 ZIP: 95616  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Macintosh 6.0.7  
 SOFTWARE: MicrosoftWord 4.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US91/01746  
 FILING DATE: 19910314  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/615,784  
 FILING DATE: 14-NOV-1990  
 APPLICATION NUMBER: 07/567,373  
 FILING DATE: 13-AUG-1990  
 APPLICATION NUMBER: 07/494,106  
 FILING DATE: 16-MAR-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lassen, Elizabeth  
 REGISTRATION NUMBER: 31,845  
 NAME: Donna E. Scherer  
 REGISTRATION NUMBER: 34,719  
 REFERENCE/DOCKET NUMBER: CGNE 69-3 WO  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (916) 753-6313  
 TELEFAX: (916) 753-1510  
 TELEX: 356370 CGNE  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 398 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US91-01746-20

Query Match 88.6%; Score 1698; DB 5; Length 398;  
 Best Local Similarity 88.2%; Pred. No. 6, 3e-159; Mismatches 15; Indels 0; Gaps 0;

Qy 8 SKEVENLKPKFMPREHVQVTHSMPPQKIEFKSLDNWAENILVHLKPVEKWCWQDF 67  
 Db 314; Conservative Matches 314; Mismatches 27; Indels 0; Gaps 0;

Qy 8 SKEVENLKPKFMPREHVQVTHSMPPQKIEFKSLDNWAENILVHLKPVEKWCWQDF 67  
 Db 43 SKEVESLKPKFPPKEVHQVHSMPQKIEFKSLDNWAENILVHLKPVEKWCWQDF 102

Qy 68 GFIYTSQERATFISHGNTARQAKEHGDIAKQICGTTAADERKRHETAYTKIVEKLFIED 127  
 Db 103 GFIYTSQERATFISHGNTARQAKEHGDIAKQICGTTAADERKRHETAYTKIVEKLFIED 162

Qy 128 SPTSWA1WTRWAAENRHGDLINKYLSSGVDMDPTEKTYLIGSGMDPRTENSPYL 187  
 Db 163 SPTSWA1WTRWAAENRHGDLINKYLSSGVDMDPTEKTYLIGSGMDPRTENSPYL 222

Qy 188 GFIYTSQERATFISHGNTARQAKEHGDIAKQICGTTAADERKRHETAYTKIVEKLFIED 247  
 Db 223 GFIYTSQERATFISHGNTARQAKEHGDIAKQICGTTAADERKRHETAYTKIVEKLFIED 282

Qy 248 PGDTVLAFADMRRKKISMPAHLYMDGRDDNLFDHFSAYAORLGVTAKDYADILEFLVGR 307  
 Db 283 PGDTVMFAFDMRRKKISMPAHLYMDGRDLSFNSAQRQLGVTAKDYADILEFLVGR 342

Qy 308 WKVDKTLGLSAECQAKDYVCPLPPIRRLERQGRAKEATMPESWIFDQVKL 363  
 Db 343 WKTESLGLSGEGNKAQEYLCLGLTPRIRRLDRAQAKKGKVPSWIDOREVQL 398

Qy 308 WVKDKTGLGSAGSGQKADYVCLCPIRRLEAQGRAKEAPTPMPFSWLFDRQVKL 363  
 Db 343 WKIESLTGLSGEGNKAQEYLCLGLTPRIRLDERAQARAKKGPKVPSMIDREVQL 398

RESULT 14  
 US-08-539-798-4  
 Sequence 4, Application US/08539798  
 Patent No. 5614400  
 GENERAL INFORMATION:  
 APPLICANT: CAHOON, Edgar B.  
 ADDRESS: Pioneer Hi-Bred International, Inc.  
 STREET: 700 Capital Square, 400 Locust Street  
 CITY: Des Moines  
 STATE: Iowa  
 COUNTRY: US  
 ZIP: 50309  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/539,798  
 FILING DATE:  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/329,560  
 FILING DATE: 26-OCT-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Yates, Michael E.  
 REGISTRATION NUMBER: 36,063  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (515) 248-4800  
 TELEFAX: (515) 248-4844  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 385 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 US-08-539-798-4

Query Match 68.7%; Score 1316; DB 1; Length 385;  
 Best Local Similarity 67.1%; Pred. No. 2, 5e-121;  
 Matches 247; Conservative 46; Nismatches 55; Indels 20; Gaps 4;

Qy 13 NUKKPFMPREYHQ-----VTHSMP-----VTHSMP-----VTHSMP-----  
 Db 17 NMFTRIAPPQGRVRSKVSMASTLHASPLVFDKLKAGRPEDFLNSLEGWARDNLVHL 76  
 Qy 56 KVEKCKWQPODFLPPDASDFGDFQEVRELERAKEIPDDYFVVLGDMTEALPTYQTM 115  
 Db 77 KSVENSPQDQFLPDTDAFQKEMERAKDIPDVEYVVLGDMTEALPTYQTM 136  
 Qy 116 NTLDGVREDTGASPTSWA1WTRAWTAENRHGDLNLKYLGSRVDMROIEKTQYLGS 175  
 Db 137 NRCGDIKDTGQAQTSWATWTRAWTAENRHGDLNLKYLGSRVDMROIEKTQYLGS 196  
 Qy 176 GMDPRTENSPLYGLFIYTSQERATEFISHNTAQAKEYGDIQCTGTADEKRHET 235  
 Db 197 GMDTKTENCPYGFYTSQERATEFISHNTAQAKEYGDIQCTGTADEKRHET 235  
 Qy 236 YTKIVEKLFEDPDGTWLAFAIDMRKKTSMPAHLYMDGRDNLNEDPHFSAVQRQSLVYTAK 295  
 Db 257 YTKIVEKLFEDPDGTWLAFAIDMRKKTSMPAHLYMDGRDNLNEDPHFSAVQRQSLVYTAK 295

Qy 296 DYADILEFLYGRWKVDLTLGSAEGQKAQDYYCRLPPRIRLBEAQGRAKEAPTPM-F 353  
 Db 317 DYCDLFLVQKWNVAKMTGSGEGRKAQEYVCSLAAKIRVEEKVQGKEKKA-VLPVAF 375

Qy 354 SWIFDROY 361  
 Db 376 SWIFNRQI 383

RESULT 15  
 US-08-329-560-4  
 Sequence 4, Application US/08329560  
 Patent No. 565402  
 GENERAL INFORMATION:  
 APPLICANT: CAHOON, Edgar B.  
 ADDRESS: Pioneer Hi-Bred International, Inc.  
 STREET: 700 Capital Square, 400 Locust Street  
 CITY: Des Moines  
 STATE: Iowa  
 COUNTRY: US  
 ZIP: 50309  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/329,560  
 FILING DATE: 26-OCT-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Yates, Michael E.  
 REGISTRATION NUMBER: 36,063  
 REFERENCE/DOCKET NUMBER: 0284US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (515) 248-4800  
 TELEFAX: (515) 248-4844  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 385 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 US-08-329-560-4

Query Match 68.7%; Score 1316; DB 1; Length 385;  
 Best Local Similarity 67.1%; Pred. No. 2.5e-121;  
 Matches 247; Conservative 46; Nismatches 55; Indels 20; Gaps 20;

Qy 13 NUKKPFMPREYHQ-----VTHSMP-----VTHSMP-----VTHSMP-----  
 Db 17 NMFTRIAPPQGRVRSKVSMASTLHASPLVFDKLKAGRPEDFLNSLEGWARDNLVHL 76  
 Qy 56 KVEKCKWQPODFLPPDASDFGDFQEVRELERAKEIPDDYFVVLGDMTEALPTYQTM 115  
 Db 77 KSVENSPQDQFLPDTDAFQKEMERAKDIPDVEYVVLGDMTEALPTYQTM 136  
 Qy 116 NTLDGVREDTGASPTSWA1WTRAWTAENRHGDLNLKYLGSRVDMROIEKTQYLGS 175  
 Db 137 NRCGDIKDTGQAQTSWATWTRAWTAENRHGDLNLKYLGSRVDMROIEKTQYLGS 196  
 Qy 176 GMDPRTENSPLYGLFIYTSQERATEFISHNTAQAKEYGDIQCTGTADEKRHET 235  
 Db 197 GMDTKTENCPYGFYTSQERATEFISHNTAQAKEYGDIQCTGTADEKRHET 235  
 Qy 236 YTKIVEKLFEDPDGTWLAFAIDMRKKTSMPAHLYMDGRDNLNEDPHFSAVQRQSLVYTAK 295  
 Db 257 YTKIVEKLFEDPDGTWLAFAIDMRKKTSMPAHLYMDGRDNLNEDPHFSAVQRQSLVYTAK 295

Db	257	YTKIVEKLAEDPDTTVIAESDMRMKKIQMPAHAMYDGSDDMLFKHFTAVSQIGVYSAW	316
QY	296	DYADLLEFLYGRWKVYDKLTLGSAEGOKAQDYVCRUPLPRIRRLEERAQGRAKEAPPTMP--F	353
Db	317	DYCDLDFLVKWNVAKMTGLSGBGRKAQEYVCSSLAAKIRVEEKVQGKEKA-VLPVAF	375
QY	354	SWIFBRQV	361
Db	376	SWIFRQI	383

Search completed: March 7, 2003, 03:11:02  
Job time: 20 secs



PF	08-JUN-2000; 2000MO-US15741.	XX	28-MAY-1998 (first entry)
XX	09-JUN-1999; 99US-0328550.	XX	Ricinus communis desaturase from clone pCGN3230.
PR	(BRCO-) BROOKHAVEN SCI ASSOC LLC.	DE	Ricinus communis; castor bean; delta-9 desaturase; oilseed;
PA		KW	Ricinus communis; castor bean; delta-9 desaturase; oilseed;
XX		KW	fatty acid saturation.
PI	Shanklin J;	XX	Ricinus communis.
XX	WPI; 2001-091202/10.	OS	Ricinus communis.
DR	DR N-PSDB; AACB4531.	XX	US5723555-A.
XX	New mutant castor Delta9-18:0-Acy1 Carrier Protein desaturase, useful in producing commercially valuable products, e.g. vegetable oils useful in human nutrition or as industrial chemicals	PN	US5723555-A.
PT		XX	03-MAR-1998.
PT		PD	03-MAR-1998.
XX		XX	06-JUN-1995; 95US-0471791.
PS	Examples; Fig 1; 53pp; English.	PF	06-JUN-1995; 95US-0471791.
XX		XX	16-SEP-1991; 91US-072762.
CC	The invention relates to a new mutant castor Delta9-18:0-acyl carrier protein (ACP) desaturase that has one or more amino acid substitutions selected from: (a) Ala for Met at residue 114; (b) Arg for Thr at residue 117; (c) Gly for Ileu at residue 118; (d) Val for Pro at residue 179; (e) Val for Thr at residue 181; (f) Leu for Gly at residue 188; and (g) Phe for Thr at residue 181. The mutant castor Delta9-18:0-ACP desaturase is useful in producing commercially useful products, such as vegetable oils rich in monounsaturated fatty acids. Such vegetable oils are important in human nutrition and can be used as renewable sources of industrial chemicals. A method for specifically altering a function of a protein through directed mutagenesis is also provided. The method can be used for altering enzymatic functions, binding functions or structural functions of the castor desaturase enzyme. The method is also useful for manipulating the physical properties and commercial uses of conventional plant oils. The present sequence represents the mature castor enzyme.	PR	16-MAR-1990; 90US-0414106.
CC		CC	13-AUG-1990; 90US-0567373.
CC		PR	14-NOV-1990; 90US-065784.
CC		PR	14-MAR-1991; 91US-051746.
CC		PR	06-JUN-1995; 95US-0471791.
CC		XX	06-JUN-1995; 95US-0471791.
CC		PA	(CALGENE INC.
CC		PA	Knauf VC, Thompson GA;
CC		PI	WPI; 1998-175544/16.
CC		DR	N-PSDB; AAV1252.
CC		XX	DNA encoding plant delta-9 desaturase protein - having amino acid sequence of <i>Carthamus tinctorius</i> desaturase, useful for, e.g. producing oilseeds with modified levels of fatty acid saturation.
CC		PT	DNA encoding plant delta-9 desaturase protein - having amino acid sequence of <i>Carthamus tinctorius</i> desaturase, useful for, e.g. producing oilseeds with modified levels of fatty acid saturation.
XX		PT	
PS	Sequence: Fig 1; 53pp; English.	XX	
PS	Claim 7; Column 59-60; 87pp; English.	XX	
XX		XX	The present sequence represents a <i>Ricinus communis</i> desaturase from clone pCGN3230. The present invention describes a recombinant DNA construct comprising a DNA sequence encoding a plant Delta-9 desaturase protein. The present invention also provides a method of modifying fatty acid composition in a host plant cell from a given fatty acid saturation to a different fatty acid saturation, comprising growing a host plant cell containing recombinant DNA sequence which encodes a plant desaturase under the control of regulatory elements functional in the plant cell during lipid accumulation. Also, oilseeds having a modified level of fatty acid saturation and oils produced from such oilseeds.
PS	Sequence: Fig 1; 53pp; English.	XX	
PS	Sequence: Fig 1; 53pp; English.	XX	
Query	Match	100.0%	Score 1916; DB 19; Length 363;
Best	Local Similarity	100.0%	Pred. No. 1.2e-171; Mismatches 0; Indels 0; Gaps 0;
Matches	363;	Conservative 0;	
Query	1 ASTLKSGSKKEVNLKPKMPREHVQVTHSMPQKIEFKSLDNWAENILVHLKPEK 60	CC	The present sequence represents a <i>Ricinus communis</i> desaturase from clone pCGN3230. The present invention describes a recombinant DNA construct comprising a DNA sequence encoding a plant Delta-9 desaturase protein. The present invention also provides a method of modifying fatty acid composition in a host plant cell from a given fatty acid saturation to a different fatty acid saturation, comprising growing a host plant cell containing recombinant DNA sequence which encodes a plant desaturase under the control of regulatory elements functional in the plant cell during lipid accumulation. Also, oilseeds having a modified level of fatty acid saturation and oils produced from such oilseeds.
Db	1 ASTLKSGSKKEVNLKPKMPREHVQVTHSMPQKIEFKSLDNWAENILVHLKPEK 60	CC	
Query	61 CWQODFLPDPASGDFDQEVRERAKTPDDYFVYLVGMITEALPTYQTMNLNTDG 120	CC	
Db	61 CWQODFLPDPASGDFDQEVRERAKTPDDYFVYLVGMITEALPTYQTMNLNTDG 120	CC	
Query	121 VRDENGASPTSWAINTRANTAEENRHGDLNLNKYLIGSGMDPR 180	CC	
Db	121 VRDENGASPTSWAINTRANTAEENRHGDLNLNKYLIGSGMDPR 180	CC	
Query	181 TENSPLYGLFIYTSFQERATFISHGNTARQAEKGDKIQLAQICGTIAADEKRHETAYTKV 240	CC	
Db	181 TENSPLYGLFIYTSFQERATFISHGNTARQAEKGDKIQLAQICGTIAADEKRHETAYTKV 240	CC	
Query	241 EKLFELIDPDGTVALPADMMRKKISMPAHLMYGRDNLFDFHSAVQLGVYTAQDYADI 300	CC	
Db	241 EKLFELIDPDGTVALPADMMRKKISMPAHLMYGRDNLFDFHSAVQLGVYTAQDYADI 300	CC	
Query	301 LEEFLYGRWKVDKLTGLSAEQQKAQDYVCRUPPRIRRLLEERAQGRAKEAFTMPFSWIFDQ 360	CC	
Db	301 LEEFLYGRWKVDKLTGLSAEQQKAQDYVCRUPPRIRRLLEERAQGRAKEAFTMPFSWIFDQ 360	CC	
Query	361 VKL 363	CC	
Db	361 VKL 363	CC	
RESULT 2			
AAW44350			
ID	AAW44350 standard; Protein: 396 AA.		
XX			
AC	AAW44350;		



Matches	326;	Conservative	24;	Mismatches	13;	Indels	0;	Gaps	0;
Qy	1	ASTLKSQSKKEVNKKPMPPEVYVQVTHSPQKIEFKLIFSKLDNVAEENILVHLKPVEK	60	XX	XX	XX	XX	XX	XX
Db	29	ASTLRSQSKKEVNKKPMPPEVYVQVTHSPQKIEFKLIFSKLDNVAEENILVHLKPVEK	88	CC	CC	CC	CC	CC	CC
Qy	61	CNQPODFLPDPASDGFEDQVRLRERAKEIPDDYFVVLGMDITEALPVTQYTMNLTLDG	120	CC	CC	CC	CC	CC	CC
Db	89	CNQPODFLPDPASDGFEDQVRLRERAKEIPDDYFVVLGMDITEALPVTQYTMNLTLDG	148	CC	CC	CC	CC	CC	CC
Qy	121	VRDETGAASPTSAWVTRAWTAENRHDLLNLYLSSGRVMDRQTEKTIOLIGSGMDPR	180	CC	CC	CC	CC	CC	CC
Db	149	VRDETGAASPTSAWVTRAWTAENRHDLLNLYLSSGRVMDRQTEKTIOLIGSGMDPR	208	CC	CC	CC	CC	CC	CC
Qy	181	TENSPYLCFIVNSQERATEISHGNTARQAKHGTDLKLAQIGTIAADEKPHETATKIV	240	XX	XX	XX	XX	XX	XX
Db	209	TENSPYLCFIVNSQERATEISHGNTARLAKHGDIKLAQIGTGMIADEKPHETATKIV	268	Sequence	391 AA;	Query	91.5%	Score	1753;
Qy	241	EKLEFIDPDGTIVLAFADMMRKTKTSIAPAHLYMGRDDNLFDHESAVAOQLGYTTAKYADI	300	Match	DB 19;	Best	89.8%	DB	Length 391;
Db	269	EKLEFIDPDGTIVLAFADMMRKTKTSIAPAHLYMGRDDNLFDHESAVAOQLGYTTAKYADI	328	Local	Prod. No. 2.9e-156;	Local	89.8%	Indels	0;
Qy	301	LEFLVGRKVKDVKITGLSABGQKAQDYCRLPPRIRLDEERAGRAKEAPTMFWSWIFDQ	360	Matches	Mismatches	Conservative	24;	Gaps	0;
Db	329	LEFLVGRKVKDVKITGLSABGQKAQDYCRLPPRIRLDEERAGRAKEAPTMFWSWIFDQ	388	326;	3	326;	24;	Indels	0;
Qy	361	VKL 363		Qy	1	ASPLKSGSKEVENLKKPMPPEVYVQVTHSPQKIEFKLIFSKLDNVAEENILVHLKPVEK	60	Qy	1
Db	389	VLL 391		Db	29	ASPLRSGSKEVENLKKPMPPEVYVQVTHSPQKIEFKLIFSKLDNVAEENILVHLKPVEK	88	Db	29
RESULT 5				Qy	61	CNQPODFLPDPASDGFEDQVRLRERAKEIPDDYFVVLGMDITEALPVTQYTMNLTLDG	120	Qy	61
TD				Db	89	CNQPODFLPDPASDGFEDQVRLRERAKEIPDDYFVVLGMDITEALPVTQYTMNLTLDG	148	Db	89
AAW37939				Qy	121	VRDETGAASPTSAWVTRAWTAENRHDLLNLYLSSGRVMDRQTEKTIOLIGSGMDPR	180	Qy	121
AAW37939				Db	149	VRDETGAASPTSAWVTRAWTAENRHDLLNLYLSSGRVMDRQTEKTIOLIGSGMDPR	208	Db	149
AC				Qy	181	TENSPYLCFIVNSQERATEISHGNTARQAKHGTDLKLAQIGTIAADEKPHETATKIV	240	Qy	181
XX				Db	209	TENSPYLCFIVNSQERATEISHGNTARLAKHGDIKLAQIGTGMIADEKPHETATKIV	268	Db	209
DT				Qy	241	EKLEFIDPDGTIVLAFADMMRKTKTSIAPAHLYMGRDDNLFDHESAVAOQLGYTTAKYADI	300	Qy	241
21-AUG-1998				Db	269	EKLEFIDPDGTIVLAFADMMRKTKTSIAPAHLYMGRDDNLFDHESAVAOQLGYTTAKYADI	328	Db	269
XX				Qy	301	LEFLVGRKVKDVKITGLSABGQKAQDYCRLPPRIRLDEERAGRAKEAPTMFWSWIFDQ	360	Qy	301
DE				Db	329	LEFLVGRKVKDVKITGLSABGQKAQDYCRLPPRIRLDEERAGRAKEAPTMFWSWIFDQ	388	Db	329
Amino acid sequence of the soybean seed stearoyl-ACP desaturase.				Qy	361	VKL 363		Qy	361
XX				Db	389	VLL 391		Db	389
XX				RESULT 6					
XX				ID	AARI4188				
Key				XX	AARI4188;				
Peptide				AC					
FT				XX					
Protein				DT	11-DEC-1991 (first entry)				
FT				C.	tinctorius delta9 desaturase from pCGN274.				
				DE					
				XX					
				Desaturase; fatty acid; saturation; chill tolerance; lipid;					
				KW					
				herbicide.					
				XX					
				OS					
				Carthamus tinctorius.					
				XX					
				Location/Qualifiers					
				XX					
				Key		Location/Qualifiers			
				XX					
				Peptide					
				XX					
				FT	1..33				
				FT	transit_peptide				
				FT	34..396				
				FT	protein				
				FT	/label= mature_protein				
				XX					
				XX					
				W0913972-A.					
				XX					

RESULT 7 AAR22048

Qy	361	VKL	363	Db	214	TENSPYLGFITYSFQERATEVSHGNTAHRHKDHDVKLAQICGTTIASDEKRHETAYTKIV	273
Db	394	VKL	396	Qy	241	EKLFEIDPDGTVLAFADNMIRKK1SMPAHILYDGRDDNLFDHESAVAOQLGVYTAKDYADI	300
				Db	274	EKLFEIDPDGTVLAFADNMIRKK1SMPAHILYDGRDDNLFDHESAVAOQLGVYTAKDYADI	333
RESULT 8				Qy	301	LEFLVGRKVKVDKLTGLSAEGOKAQDYVQLPPRIRRLEQRAQRAKEAPTMPESWIDRQ	360
AAR54033				Db	334	LEFLVGRKVKVADLTGLSEGRKAQDYVQLPPRIRRLEQRAKEPVPVPSWIDRQ	393
ID	AAR54033	standard; Protein;	396 AA.	Qy	361	VKL	363
XY				Db	394	VKL	396
AC							
XX							
DT	01-DEC-1994	(first entry)					
XX							
DE	Sequence encoding desaturase enzyme.						
XX							
KW	Synthase; plants; oil; seed; fatty acids; gene expression;						
XX							
OS	biosynthesis; ss.						
XX							
C.	tinctorius.						
XX							
PN	W09410189-A.						
XX							
PD	11-MAY-1994.						
XX							
PF	02-NOV-1993;	93WO-US10526.					
XX							
PR	02-NOV-1992;	92US-0971182.					
XX							
PA	(CALJ ) CALGENE INC.						
XX							
PI	Knauf VC, Thompson GA;						
XX							
DR	WPI: 1994-167378/20.						
XX							
N-PSDB;	AAQ64033.						
XX							
PT	DNA constructs encoding beta-ketoacyl-ACP synthase - useful to						
XX							
PT	modify the oil content of seeds, e.g. for dietary purposes						
XX							
PS	Disclosure: Figure 10; 85pp; English.						
XX							
CC	Higher plants appear to share a common metabolic pathway for the						
CC	synthesis of fatty acids. Genes encoding synthase proteins may be						
CC	used in nucleic acid constructs to modulate the amount of synthase						
CC	activity in a host cell. Nucleic acid constructs may also be						
CC	designed to decrease the expression of a synthase protein, i.e.,						
CC	constructs containing anti-sense synthase sequences. The constructs						
CC	allow the generation of plants bearing seeds which have enhanced oil						
CC	yields and/or altered compositions of oils. The production of						
CC	common plant unsaturated fatty acids is catalyzed by a desaturase.						
CC	Oleic, linoleic and alpha-linoleic acids found in storage						
CC	triglycerides are produced from the desaturation of stearoyl-ACP to						
CC	form oleoyl-ACP.						
XX							
SO	Sequence 396 AA:						
Query Match	91.4%	Score 1752;	DB 15;	Length 396;			
Best Local Similarity	90.18;	Pred No. 3.7e-156;					
Matches 327;	Conservative	18; Mismatches 18;	Indels 0;	Gaps 0;			
Qy	1	ASTLKGSKVEVNLKKPFMPPREHVQVTHSMPPOKIEFKSLDNWAEENILVHLKPVK	60				
Db	34	ASTLGSSTPKVDNAKKPFPQPPREHVQVTHSMPPOKIEFKSIRGWAENILVHLKPVK	93				
Qy	61	CWQDQFLPDA5DGEQPLRERAKEPDDPFVVLGMDTPEALPTYQMLNLDG	120				
Db	94	CWQADQFLPDBASEGDFQELKARAKEPDDPFVVLGMDTPEALPTYQMLNLDG	153				
Qy	121	VRDETAGSPSTSVAINTRTAENRHDLINKLYLSSGRYDVMROIEKTIQYLIGSGMDPR	180				
Db	154	VRDETAGSLTETWAVNTRAWTAENRHDLINKLYLSSGRYDVMROIQKTIQYLIGSGMDPR	213				
Qy	181	TENSPYLGFITYSFQERATEVSHGNTAHRHKDHDVKLAQICGTTAADEKRHETAYTKIV	240				

SQ	Sequence	396 AA;	91.4%;	Score 1752;	DB 19;	Length 396;	99US-0132407.
Best Local Similarity	90.1%;	Pred. No. 3.7e-156;					99US-0132484.
Matches	322;	Conservative	18;	Mismatches	18;	Indels	0;
Gaps	0;						99US-0132485.
PR	30-APR-1999;						99US-0132486.
PR	04-MAY-1999;						99US-0132487.
PR	05-MAY-1999;						99US-0132488.
PR	06-MAY-1999;						99US-0132489.
PR	07-MAY-1999;						99US-0132863.
PR	11-MAY-1999;						99US-0134256.
PR	14-MAY-1999;						99US-0134218.
PR	14-MAY-1999;						99US-0134219.
PR	14-MAY-1999;						99US-0134221.
PR	14-MAY-1999;						99US-0134310.
PR	18-MAY-1999;						99US-0134768.
PR	19-MAY-1999;						99US-0134941.
PR	20-MAY-1999;						99US-0135124.
PR	21-MAY-1999;						99US-0135353.
PR	24-MAY-1999;						99US-0135629.
PR	24-MAY-1999;						99US-0136021.
PR	27-MAY-1999;						99US-0136397.
PR	28-MAY-1999;						99US-0136782.
PR	01-JUN-1999;						99US-0137222.
PR	03-JUN-1999;						99US-0137528.
PR	04-JUN-1999;						99US-0137502.
PR	04-JUN-1999;						99US-0137724.
PR	08-JUN-1999;						99US-0138094.
PR	10-JUN-1999;						99US-0138540.
PR	10-JUN-1999;						99US-0138847.
PR	14-JUN-1999;						99US-0139119.
PR	16-JUN-1999;						99US-0139452.
PR	16-JUN-1999;						99US-0139453.
PR	17-JUN-1999;						99US-0139492.
PR	18-JUN-1999;						99US-0139454.
PR	18-JUN-1999;						99US-0139455.
PR	18-JUN-1999;						99US-0139456.
PR	18-JUN-1999;						99US-0139457.
PR	18-JUN-1999;						99US-0139458.
PR	18-JUN-1999;						99US-0139459.
PR	18-JUN-1999;						99US-0139460.
PR	18-JUN-1999;						99US-0139461.
PR	18-JUN-1999;						99US-0139462.
PR	18-JUN-1999;						99US-0139463.
PR	18-JUN-1999;						99US-0139464.
PR	18-JUN-1999;						99US-0139750.
PR	18-JUN-1999;						99US-0139763.
PR	21-JUN-1999;						99US-0139817.
PR	23-JUN-1999;						99US-0140353.
PR	23-JUN-1999;						99US-0140354.
PR	24-JUN-1999;						99US-0140695.
PR	28-JUN-1999;						99US-0140823.
PR	29-JUN-1999;						99US-0140991.
PR	30-JUN-1999;						99US-0141287.
PR	01-JUL-1999;						99US-0141842.
PR	01-JUL-1999;						99US-0142154.
PR	02-JUL-1999;						99US-0142055.
PR	06-JUL-1999;						99US-0142390.
PR	08-JUL-1999;						99US-0142803.
PR	09-JUL-1999;						99US-0142920.
PR	12-JUL-1999;						99US-0142977.
PR	13-JUL-1999;						99US-0143542.
PR	14-JUL-1999;						99US-0143624.
PR	15-JUL-1999;						99US-0144005.
PR	16-JUL-1999;						99US-0144085.
PR	16-JUL-1999;						99US-0144086.
PR	19-JUL-1999;						99US-0144334.
PR	19-JUL-1999;						99US-0144335.
PR	20-JUL-1999;						99US-0144352.
PR	20-JUL-1999;						99US-0144632.
PR	21-JUL-1999;						99US-0144814.
PR	21-JUL-1999;						99US-0145086.

PR	21-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160767.
PR	22-JUL-1999;	99US-0145085.	PR	21-OCT-1999;	99US-0160768.
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160770.
PR	22-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160814.
PR	22-JUL-1999;	99US-0145192.	PR	21-OCT-1999;	99US-0160815.
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160980.
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.
PR	23-JUL-1999;	99US-0145224.	PR	22-OCT-1999;	99US-0160989.
PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.
PR	27-JUL-1999;	99US-0145913.	PR	25-OCT-1999;	99US-0161405.
PR	27-JUL-1999;	99US-0145918.	PR	26-OCT-1999;	99US-0161406.
PR	28-JUL-1999;	99US-0145919.	PR	26-OCT-1999;	99US-0161359.
PR	02-AUG-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161360.
PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146388.	PR	28-OCT-1999;	99US-0161920.
PR	03-AUG-1999;	99US-0147038.	PR	28-OCT-1999;	99US-0161992.
PR	04-AUG-1999;	99US-0147204.	PR	28-OCT-1999;	99US-0161993.
PR	04-AUG-1999;	99US-0147302.	PR	29-OCT-1999;	99US-0162142.
PR	05-AUG-1999;	99US-0147192.	Query	Match	90.4%;
PR	05-AUG-1999;	99US-0147260.	Query	Best Local Similarity	89.4%;
PR	06-AUG-1999;	99US-0147303.	Matches	Conservative	89.4%;
PR	06-AUG-1999;	99US-0147416.	PR	22	Mismatches
PR	09-AUG-1999;	99US-0147493.	PR	16	Indels
PR	09-AUG-1999;	99US-0147935.	PR	0	Gaps
PR	10-AUG-1999;	99US-0148171.	PR	4	
PR	11-AUG-1999;	99US-0148319.	PR	4	
PR	12-AUG-1999;	99US-0148341.	PR	4	
PR	13-AUG-1999;	99US-0148565.	PR	4	
PR	13-AUG-1999;	99US-0148684.	PR	4	
PR	16-AUG-1999;	99US-0149363.	PR	4	
PR	17-AUG-1999;	99US-0149475.	PR	4	
PR	18-AUG-1999;	99US-0149426.	PR	4	
PR	20-AUG-1999;	99US-0149722.	PR	4	
PR	20-AUG-1999;	99US-0149723.	PR	4	
PR	20-AUG-1999;	99US-0149929.	PR	4	
PR	23-AUG-1999;	99US-0149902.	PR	4	
PR	23-AUG-1999;	99US-0149930.	PR	4	
PR	25-AUG-1999;	99US-0150566.	PR	4	
PR	26-AUG-1999;	99US-0150884.	PR	4	
PR	27-AUG-1999;	99US-0151065.	PR	4	
PR	27-AUG-1999;	99US-0151066.	PR	4	
PR	30-AUG-1999;	99US-0151080.	PR	4	
PR	31-AUG-1999;	99US-0151303.	PR	4	
PR	01-SEP-1999;	99US-0151438.	PR	4	
PR	07-SEP-1999;	99US-0151930.	PR	4	
PR	10-SEP-1999;	99US-0152363.	PR	4	
PR	13-SEP-1999;	99US-0153070.	PR	4	
PR	15-SEP-1999;	99US-0154018.	PR	4	
PR	16-SEP-1999;	99US-0154039.	PR	4	
PR	22-SEP-1999;	99US-0155139.	PR	4	
PR	23-SEP-1999;	99US-0155486.	PR	4	
PR	24-SEP-1999;	99US-0155659.	PR	4	
PR	28-SEP-1999;	99US-0156458.	PR	4	
PR	29-SEP-1999;	99US-0156596.	PR	4	
PR	12-OCT-1999;	99US-0156817.	PR	4	
PR	13-OCT-1999;	99US-0157171.	PR	4	
PR	05-OCT-1999;	99US-015753.	PR	4	
PR	06-OCT-1999;	99US-015775.	PR	4	
PR	07-OCT-1999;	99US-0157865.	PR	4	
PR	14-OCT-1999;	99US-0158339.	PR	4	
PR	14-OCT-1999;	99US-0158322.	PR	4	
PR	14-OCT-1999;	99US-0158369.	PR	4	
PR	13-OCT-1999;	99US-0158293.	PR	4	
PR	13-OCT-1999;	99US-0159294.	PR	4	
PR	13-OCT-1999;	99US-0157295.	PR	4	
PR	14-OCT-1999;	99US-0158339.	PR	4	
PR	14-OCT-1999;	99US-0159330.	PR	4	
PR	14-OCT-1999;	99US-0159331.	PR	4	
PR	14-OCT-1999;	99US-0159638.	PR	4	
PR	18-OCT-1999;	99US-0159584.	PR	4	
PR	21-OCT-1999;	99US-0160741.	PR	4	
			RESULT	1.1	
			ID	ABP92108	
			ABP92108 standard; Protein;	401 AA.	
			XX	AC	
			XX	XX	
			XX	DT	
			XX	XX	
			XX	DE	
			XX	Herbicidal; plant; agriculture; herbicide.	
			XX	OS	
			XX	Arabidopsis thaliana.	
			PN	WO200210210-A2.	
			XX	XX	
			PD	07-FEB-2002.	
			XX	XX	
			PR	28-AUG-2001;	2001WO-EPP0892.
			XX	XX	
			PR	28-AUG-2001;	2001WO-EPP0892.
			XX	XX	
			PA	(FARB ) BAYER AG.	
			XX	PA	
			PI	Tietjen K, Weidler M;	

XX WPI; 2002-269010/31.  
 XX  
 PT Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms -  
 PT  
 PT  
 PS Claim 5; SEQ ID NO 1319; 261pp + Sequence Listing; English.  
 XX  
 CC The invention relates to identifying target proteins (ABB0790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.  
 XX  
 Sequence 401 AA;

Query Match 90.4%; Score 1733; DB 23; Length 401;  
 Best Local Similarity 89.4%; Pred. No. 2.3e-154;  
 Matches 322; Conservative 22; Mismatches 16; Indels 0; Gaps 0;  
 Qy 4 LKSGSKEVENLKKPMPMPREYHVQYTHSMPPQKIEIFKSLDNWAEEENILVHLKPVKEKMQ 63  
 Db 42 LSSGPKVESELKKPMPFPREYHVQVLSHSMPPQKIEIFKSMENAEENLILHLKDVKEKMQ 101  
 Qy 64 PQDFLDPDPSDGFDEQYRELERAKEIPTDDYFVVLGDMTEALPTYQTMNLNTLGVRD 123  
 Db 102 PQDFLDPDPSDGFDEQYRELERAKERELPDDYFVVLGDMTEALPTYQTMNLNTLGVRD 161  
 Qy 124 ETGASPTSWALWTRATAENRHGDLNLKLYLGSRVDMRQIEKTIQYLGSGMQPRTE 183  
 Db 162 ETGASPTSWALWTRATAENRHGDLNLKLYLGSRVDMRQIEKTIQYLGSGMQPRTE 221  
 Qy 184 SPYLGFIYTSQFQERATFISHGNTAROKEHCDIKLAQICGTTAADEKRHETAYTKIVEKL 243  
 Db 222 NYPLGFIYTSQFQERATFISHGNTAROKEHCDIKLAQICGTTAADEKRHETAYTKIVEKL 281  
 Qy 244 FEIDPGTVALFADMRKKISMPAHLYMDGRDDNLFHSAVQAORLGVYPAKDYADILEF 303  
 Db 282 FEIDPGTVALFADMRKKISMPAHLYMDGRDNLFHSAVQAORLGVYPAKDYADILEF 341  
 Qy 304 LYGRWKVDKLTLGSLAEGQKAQDYCVRLPRIRRLEBRAQGRAKEAPTMPSWIFDQVKL 363  
 Db 342 LYGRWKVQDFTGLSGEGCNKKAQDYLCGLAPRKRLDERAQAKKGPKIPFSWHDREVQL 401

RESULT 12

ABB07379  
 ID ABB07379 standard; Protein; 401 AA.  
 XX  
 AC ABB07379;  
 XX  
 DT 09-APR-2002 (first entry)

XX A. thaliana stearoyl-ACP desaturase (SS12) protein sequence.  
 KW SS12; Arabidopsis; pathogen; plant defence response; enzyme; plant; stearoyl-ACP desaturase; delta9 fatty acid desaturase; stearoyl-ACP; KW gene therapy.  
 XX Arabidopsis thaliana.  
 OS WO200196363-A1.  
 XX  
 PN 20-DEC-2001.  
 XX  
 PD 18-MAY-2001; 2001WO-US16134.

PR 12-JUN-2000; 2000US-210967P.

XX (BOYC-) BOYCE THOMPSON INST PLANT RES.

PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.

PA (UNIV) UNIV KANSAS STATE RES FOUND.

XX  
 PI Klessig DF, Kachroo P, Shah J;XX  
 PS Claim 8; Page 73-74; 80pp; English.

WPI: 2002-139703/18.  
 DR N-PSDB; ABA4565, ABA4566.

XX  
 PT Novel isolated nucleic acid molecule comprising SS12 gene encoding

PT stearoyl-acyl carrier protein desaturase in plants, which when reduced PT or prevented, is useful for enhancing resistance of plant to plant PT pathogens.

XX  
 PS Claim 8; Page 73-74; 80pp; English.

CC The invention relates to a novel plant gene, SS12, isolated from Arabidopsis thaliana (At) chromosome 2 at a location within 0.2 cm from marker AthB102 and 3.7 cm from marker GBF, the disruption of which is associated with altered resistance of a plant to plant pathogens or other disease causing agents. SS12 encodes a stearoyl-ACP desaturase in plants and plays a key role in modulating plant defence responses. The enzyme is a delta9 fatty acid desaturase that preferentially desaturates stearoyl-ACP (18:0 ACP). Methods using the SS12 gene are provided for enhancing the resistance of a plant to plant pathogens or other disease causing agents. Transgenic plants lacking SS12 protein, altered fatty acid metabolism or enhanced resistance to a selected plant pathogen, can be used for plant breeding or directly in agricultural or horticultural applications. SS12 DNA, RNA, or their fragments may be used as probes to detect the presence and/or expression of SS12 genes. SS12 nucleic acids may be utilized as probes in assays such as in situ hybridization; Southern hybridization; Northern hybridization and assorted amplification reactions such as PCR. Antibodies that are immunologically specific for SS12 may be utilized in affinity chromatography to isolate the SS12 protein to quantify the SS12 protein, or to immuno-precipitate SS12 from a sample containing a mixture of proteins and other biological materials. The ss12 mutants display a unique combination of defence responses that include constitutive HR and expression of PR genes and enhanced disease resistance to certain plant pathogens, and therefore can be used to improve crop and horticultural plant species by customizing the defence response. The ss12 mutants can be used to identify and isolate additional members of this disease resistance pathway. The SS12 transgenic plants are useful in conferring the SS12 phenotype to many different plant species. A plant with increased functional SS12 has additional defence response properties consistent with increased production of the SS12-associated fatty acid (FA)-derived signal molecule(s). Similarly, plants that have increased production or activity of the SS12 FA desaturase display broad resistance to various plant pathogens. The present sequence represents the A. thaliana stearoyl-ACP desaturase.

XX  
 SQ Sequence 401 AA;

Query Match 90.4%; Score 1733; DB 23; Length 401;  
 Best Local Similarity 89.4%; Pred. No. 2.3e-154;  
 Matches 322; Conservative 22; Mismatches 16; Indels 0; Gaps 0;

Qy 4 LKSGSKEVENLKKPMPMPREYHVQYTHSMPPQKIEIFKSLDNWAEEENILVHLKPVKECQWQ 63

Db 42 LSSGPKVESELKKPMPFPREYHVQVLSHSMPPQKIEIFKSMENAEENLILHLKDVKEKMQ 101

Qy 64 PQDFLDPDPSDGFDEQYRELERAKEIPTDDYFVVLGDMTEALPTYQTMNLNTLGVRD 123

Db 102 PQDFLDPDPSDGFDEQYRELERAKERELPDDYFVVLGDMTEALPTYQTMNLNTLGVRD 161

Qy 124 ETGASPTSWALWTRATAENRHGDLNLKLYLGSRVDMRQIEKTIQYLGSGMQPRTE 183

Db 162 ETGASPTSWALWTRATAENRHGDLNLKLYLGSRVDMRQIEKTIQYLGSGMQPRTE 221

Qy 184 SPYLGFIYTSQFQERATFISHGNTAROKEHCDIKLAQICGTTAADEKRHETAYTKIVEKL 243

Db 222 NYPLGFIYTSQFQERATFISHGNTAROKEHCDIKLAQICGTTAADEKRHETAYTKIVEKL 281

Qy 244 FEIDPGTVALFADMRKKISMPAHLYMDGRDDNLFHSAVQAORLGVYPAKDYADILEF 303

Db 282 FEIDPGTVALFADMRKKISMPAHLYMDGRDNLFHSAVQAORLGVYPAKDYADILEF 341

Qy 304 LYGRWKVDKLTLGSLAEGQKAQDYCVRLPRIRRLEBRAQGRAKEAPTMPSWIFDQVKL 363

Db 342 LYGRWKVQDFTGLSGEGCNKKAQDYLCGLAPRKRLDERAQAKKGPKIPFSWHDREVQL 401

XX  
 SQ Sequence 401 AA;

Query Match 90.4%; Score 1733; DB 23; Length 401;  
 Best Local Similarity 89.4%; Pred. No. 2.3e-154;  
 Matches 322; Conservative 22; Mismatches 16; Indels 0; Gaps 0;

Qy 4 LKSGSKEVENLKKPMPMPREYHVQYTHSMPPQKIEIFKSLDNWAEEENILVHLKPVKECQWQ 63

Db 42 LSSGPKVESELKKPMPFPREYHVQVLSHSMPPQKIEIFKSMENAEENLILHLKDVKEKMQ 101

Qy 64 PQDFLDPDPSDGFDEQYRELERAKEIPTDDYFVVLGDMTEALPTYQTMNLNTLGVRD 123

Db 102 PQDFLDPDPSDGFDEQYRELERAKERELPDDYFVVLGDMTEALPTYQTMNLNTLGVRD 161

Qy 124 ETGASPTSWALWTRATAENRHGDLNLKLYLGSRVDMRQIEKTIQYLGSGMQPRTE 183

Db 162 ETGASPTSWALWTRATAENRHGDLNLKLYLGSRVDMRQIEKTIQYLGSGMQPRTE 221

Qy 184 SPYLGFIYTSQFQERATFISHGNTAROKEHCDIKLAQICGTTAADEKRHETAYTKIVEKL 243

Db 222 NPYLGFIYTSQFQERATFISHGNTAROKEHCDIKLAQICGTTAADEKRHETAYTKIVEKL 281

Qy	244	FEIDPGTIVLAFADMRRKKISMPAHMLYGRDDNLFDHESAVQLGVYTTARDYADILEF	303	Db	89	CWQDPDFLPNQSSDGFEDQVKELRERAKEITLTYFVVLYGDMITEALPLTYQMLNTLDG	148
Db	282	FEIDPGTIVMAFADMRRKKISMPAHMLYGRDDNLFDHESAVQLGVYTTARDYADILEF	341	Qy	121	VRDETGASPTSWAIIWTRAWTAEEENRIGDILNKYLSSGRVDMRQLEKTIQYLGSGMDPR	180
Qy	304	LGVRWKVDKJLGLSAAESQKAQDYVCRYLPPRTRRLERQAQGRAKEAPTMPSWIFDROVKL	363	Db	149	VRDETGASLTWSAIIWTRAWTAEEENRIGDILNKYLSSGRVDMRQLEKTIQYLGSGMDPR	208
Qy	342	LGVRWKIQLDGLSGBGNKAQDYLCLGLAPTRKLDRQAARAKKGPKIPFSWIDREVQL	401	Qy	181	TENSPYLGEIYTSFQERATFISHGNTARQAKEHDIKLAQICGTTIADEKRRHETAYTKV	240
Db	342	LGVRWKIQLDGLSGBGNKAQDYLCLGLAPTRKLDRQAARAKKGPKIPFSWIDREVQL	401	Qy	209	TENSPYLGEIYTSFQERATFISHGNTARLAKENGDIKLAQICGMIAADEKRRHETAYTKV	268
RESULT 13				Qy	241	EKLFEIDPDGTIVLAFADMRRKKISMPAHMLYGRDDNLFDHFSAVQLGVYTTARDYADILEF	300
ID	AAR82024	standard; Protein; 391 AA.		Db	269	EKLFVDPDGTVMAFADMRRKKISMPAHMLYGRDDNLFDHFSAVQLGVYTTARDYADILEF	328
XX	AC	AAR82024;		Qy	301	LEFLVGRMKVVDKJLGLSAAEGQKAQDYVCRYLPPRTRRLERQAQGRAKEAPTMPSWIFDROVKL	360
XX	DT	10-APR-1996 (first entry)		Db	329	LEFLVGRMKVVEQLTLSGSGFRKAQEYVCGLPPRTRRLERQAQGRAKESTLKFWSMHDRE	388
XX	DE	Stearoyl-ACP-desaturase precursor.		Qy	361	VKL 363	
XX	KW	Stearoyl-ACP-desaturase; soybean; seed oil; vegetable oil; fatty acid; stearic acid; transgenic plant; crop improvement.		Db	389	VLL 391	
XX	OS	Glycine max cv. Wye.		RESULT 14			
XX	PH	Location/Qualifiers		AAR14190			
FT	Peptide	1..32		ID	AAR14190 standard; Protein; 398 AA.		
FT		/label= Transit_peptide		XX			
FT	protein	33..391		AC	AAR14190;		
FT		/label= Mat_protein		XX			
XX	US5443974-A.			DT	11-DEC-1991 (first entry)		
XX	PN			XX			
PD	22-AUG-1995.			DE			
XX	US5443974-A.			XX			
XX	US5443974-A.			KW			
XX	22-AUG-1995.			XX			
PD	25-MAY-1990;			KW			
XX	US5443974-A.			OS			
XX	25-MAY-1990;			XX			
PR	11-DEC-1992;			DE			
PR	920US-0995657.			XX			
PR	25-MAY-1990;			XX			
XX	900US-0529049.			KW			
PA	(DUP0 ) DU PONT DE Nemours & CO E I.			XX			
PA	PA			XX			
PI	Hitz WD, Perez-Grau L, Yadav NS;			XX			
XX	WPI: 1995-302121/39.			XX			
DR	N-PSDB; AAT00395.			PR	14-NOV-1990; 900US-0615784.		
DR				PR	16-MAR-1990; 900US-044106.		
XX				PR	13-AUG-1990; 900US-0567373.		
PT	New isolated soybean stearoyl-ACP desaturase gene - use for the prodn. of seed oil contg. altered levels of satd. and unsatd. fatty acids			PA	(CALG-) CALGENE INC.		
XX	Disclosure; Column 41-44; 25pp; English.			PA			
XX	The stearoyl-ACP-desaturase precursor (AAR82024) is the product of a cDNA clone (AAT00395) derived from soybean developing leaves. It catalyses the conversion of stearoyl-ACP to oleoyl-ACP.			XX			
CC	Expression of the mature enzyme in transgenic plants such as soybean, rapeseed, sunflower, cocoa, peanut, sunflower and corn, allows the fatty acid composition, esp. the stearic acid content, of the seed oil to be controlled.			XX			
CC	Sequence 391 AA;			XX			
CC	Query Match 89.8%; Score 1721; DB 16; Length 391;			XX			
CC	Best Local Similarity 88.7%; Pred. No. 3e-153; Mismatches 16; Indels 0; Gaps 0;			XX			
CC	Matches 322; Conserved 25; MisMatches 16; Indels 0; Gaps 0;			XX			
Qy	1	ASTLKGSKVEENLKKPFMPPREHYQVTHSMPPQKIEIFSLDNNAEENILVHLKPVEK 60		CC			
Db	29	ASTLKGSKVEENLKKPFMPPREHYQVTHSMPPQKIEIFSLDNNAEENILVHLKPVEK 88		CC			
Qy	61	CWQDPDFLPNQSSDGFEDQVKELRERAKEITLTYFVVLYGDMITEALPLTYQMLNTLDG 120		CC			

CC	See also AAQ13963-69.	CC	CDNA clones (AAT63437-38) isolated from a <i>Brassica napus</i> cv. 212/86 mid-maturation seed cDNA library. An antisense gene was constructed to generate antisense RNA homologous to both BND9 and BND11. In transgenic <i>Brassica</i> plants expressing the stearoyl-ACP desaturase antisense construct and mangosteen class I acyl-ACP thioesterase (see also AAW14795), levels of C18:0 in the seed oil may exceed 50% of total fatty acids.
XX	Sequence 398 AA:	XX	Sequence 398 AA:
SQ		Query Match 88.6%; Score 1698; DB 12; Length 398;	Query Match 88.6%; Score 1698; DB 18; Length 398;
Best Local Similarity 88.2%; Pred. No. 4.5e-151;		Best Local Similarity 88.2%; Pred. No. 4.5e-151;	
Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;		Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;	
DB	B SKEVENLKKPMPPEVHVYOTHSMPPQKIEFKSLDNNAEENTYLHLKPKVCKMOPDF 67	DB	8 SKEVENLKKPMPPEVHVYOTHSMPPQKIEFKSLDNNAEENTYLHLKPKVCKMOPDF 67
43 SKEVEKLKKPMPPEVHVYOTHSMPPQKIEFKSLDNNAEENTYLHLKPKVCKMOPDF 102		43 SKEVEKLKKPMPPEVHVYOTHSMPPQKIEFKSLDNNAEENTYLHLKPKVCKMOPDF 102	
DB	68 LPDPASDFPDEQVREERAKETIPDDYFVVLGDMITEEALPTYOTMINTLDGVDETGA 127	DB	68 LPDPASDFPDEQVREERAKETIPDDYFVVLGDMITEEALPTYOTMINTLDGVDETGA 127
103 LPDPASDFPDEQVREERAKETIPDDYFVVLGDMITEEALPTYOTMINTLDGVDETGA 162		103 LPDPASDFPDEQVREERAKETIPDDYFVVLGDMITEEALPTYOTMINTLDGVDETGA 162	
QY	128 SPTSWAIWTRAWTAEEENRGDLLNKYLISGRVDMRQIERTKIQYLIGSGMDPRTEENSPYL 187	QY	128 SPTSWAIWTRAWTAEEENRGDLLNKYLISGRVDMRQIERTKIQYLIGSGMDPRTEENSPYL 187
Db	163 SPTSWAIWTRAWTAEEENRGDLLNKYLISGRVDMRQIERTKIQYLIGSGMDPRTEENSPYL 222	Db	163 SPTSWAIWTRAWTAEEENRGDLLNKYLISGRVDMRQIERTKIQYLIGSGMDPRTEENSPYL 222
QY	188 GFIYTSFQERATFISHGNTYAROAKEHGDIIKLAQICCTIAADEKRHETAYTKIVEKLFED 247	QY	188 GFIYTSFQERATFISHGNTYAROAKEHGDIIKLAQICCTIAADEKRHETAYTKIVEKLFED 247
Db	223 GFIYTSFQERATFISHGNTYAROAKEHGDIIKLAQICCTIAADEKRHETAYTKIVEKLFED 282	Db	223 GFIYTSFQERATFISHGNTYAROAKEHGDIIKLAQICCTIAADEKRHETAYTKIVEKLFED 282
QY	248 PDGTVALAFADMRRKKISMPAHLYGCRDDNLFDFHESAVAQFLGVTYAKDADILEFLYGR 307	QY	248 PDGTVALAFADMRRKKISMPAHLYGCRDDNLFDFHESAVAQFLGVTYAKDADILEFLYGR 307
Db	283 PDGTVALAFADMRRKKISMPAHLYGCRDDNLFDFHESAVAQFLGVTYAKDADILEFLYGR 342	Db	283 PDGTVALAFADMRRKKISMPAHLYGCRDDNLFDFHESAVAQFLGVTYAKDADILEFLYGR 342
QY	308 WKVDKLTGLSAEQQKAQDYVCRLPPIRRLERAAQRAKETAPTMPSWIFDQVKL 363	QY	308 WKVDKLTGLSAEQQKAQDYVCRLPPIRRLERAAQRAKETAPTMPSWIFDQVKL 363
Db	343 WKIESLTGLSGEGNKAQEYLGGLTPPIRRLERAAQRAKGPVKFESWIDREVQL 398	Db	343 WKIESLTGLSGEGNKAQEYLGGLTPPIRRLERAAQRAKGPVKFESWIDREVQL 398
RESULT 15		RESULT 15	
AAW14798		AAW14798	
ID	AAW14798 standard; Protein: 398 AA.	ID	AAW14798 standard; Protein: 398 AA.
XX		XX	
AC	AAW14798;	AC	AAW14798;
XX		XX	
DT	03-JUL-1997 (first entry)	DT	03-JUL-1997 (first entry)
XX	Rapeseed stearoyl-ACP desaturase BND9.	XX	Rapeseed stearoyl-ACP desaturase BND9.
XX		XX	
KW	Stearoyl-ACP desaturase; rapeseed; acyl-ACP thioesterase;	KW	Stearoyl-ACP desaturase; rapeseed; acyl-ACP thioesterase;
KW	antisense; triglyceride; stearic acid; transgenic plant; oilseed;	KW	antisense; triglyceride; stearic acid; transgenic plant; oilseed;
KW	vegetable oil; mangosteen; <i>Garcinia mangifera</i> .	KW	vegetable oil; mangosteen; <i>Garcinia mangifera</i> .
OS	<i>Brassica napus</i> cv. 212/86.	OS	<i>Brassica napus</i> cv. 212/86.
XX	PN W09712047-A1.	XX	PN W09712047-A1.
XX		XX	
PD	03-APR-1997.	PD	03-APR-1997.
XX		XX	
PF	96WO-US16078.	PF	96WO-US16078.
XX		XX	
PR	95US-0537083.	PR	95US-0537083.
XX		XX	
PA	(CALJ ) CALGENE INC.	PA	(CALJ ) CALGENE INC.
XX		XX	
PI	Knauf VC, Kridl J, Lassner MW;	PI	Knauf VC, Kridl J, Lassner MW;
XX		XX	
DR	WPI; 1997-212906/19.	DR	WPI; 1997-212906/19.
N-PSDB; AA163438.		N-PSDB; AA163438.	
XX		XX	
PT	Increasing levels of stearate in plant seed triglyceride(s) using a DNA sequence encoding acyl-ACP thioesterase protein having substantial activity on C18:0 acyl-ACP substrates	PT	Increasing levels of stearate in plant seed triglyceride(s) using a DNA sequence encoding acyl-ACP thioesterase protein having substantial activity on C18:0 acyl-ACP substrates
XX		XX	
PS	Example 5: Fig7A-7C; 55pp; English.	PS	Example 5: Fig7A-7C; 55pp; English.
XX		XX	
CC	Oilseed rape stearoyl-ACP desaturases BND11 (AAW14797) and BND9 (AAW14798) each catalyze the desaturation of stearoyl-ACP (C18:0) to oleoyl-ACP (C18:1). Their amino acid sequences were deduced from	CC	Oilseed rape stearoyl-ACP desaturases BND11 (AAW14797) and BND9 (AAW14798) each catalyze the desaturation of stearoyl-ACP (C18:0) to oleoyl-ACP (C18:1). Their amino acid sequences were deduced from

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